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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:28 ; Search time 8184.59 Seconds

(without alignments)
819,445 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310
1 aatgcgataagtaatcgtga.....ggaatacccgctgaacttaa 310

Sequence: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Scoring table: 21979536 seqs, 10817449327 residues

Searched: Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCrUS_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
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Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	18	US-09-423-233-7
2	302.8	97.7	534	36	US-09-580-797-12
3	293.8	94.8	637	22	US-09-580-797-12
4	289.8	80.6	561	13	US-08-905-314-24
5	240.2	77.5	319	18	US-09-423-233-6
6	199	64.2	672	22	US-09-580-797-28
7	194.4	62.7	522	36	US-09-961-755A-8
8	194.4	62.7	522	36	US-09-961-755A-8
9	187.6	60.5	546	13	US-08-905-314-22
10	186.6	60.2	504	13	US-08-905-314-19
11	185	59.7	611	1	PCT-US98-25210-4
12	183.2	58.1	545	13	US-08-905-314-21
13	180.4	59.2	503	13	US-08-905-314-20
14	179.2	57.8	521	36	US-09-961-755A-6
15	177.8	57.4	620	22	US-09-580-797-11
16	174.2	56.2	504	18	US-09-481-293-32
17	170.8	55.1	563	22	US-09-580-797-10
18	163.8	52.8	608	1	PCT-US98-25210-3
19	141.8	45.7	392	16	US-09-241-427-3
20	140.2	45.2	599	22	US-09-580-797-37
21	139	44.8	605	1	PCT-US98-25210-1
22	138	44.5	7997	47	US-60-082-300-11599
23	136.4	44.0	597	22	US-09-580-797-35
24	136	43.9	355	18	US-09-423-233-3
25	136	43.9	617	1	PCT-US98-25210-2
26	131.4	42.4	364	18	US-09-423-233-2
27	127.2	41.0	676	22	US-09-580-797-5
28	126.6	40.8	556	14	PCT-US99-04251-7
29	126.6	40.8	556	14	US-09-423-990-7
30	125	40.3	309	18	US-09-423-233-28
31	124.4	40.1	556	13	US-08-905-314-23

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES


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Oy 61 ttgcgccgcaatattctgcgagcattgaccttcaagcgtcatltaaccctcaagcc 120
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Db 401 ttgcgccgcaatattctgcgagcattgaccttcaagcgtcatltaaccctcaagcc 460
Oy 121 ccgaggttggttggttggttggttggttggttggttggttggttggttggttggt 180
    |||||||
Db 461 ccgaggttggttggttggttggttggttggttggttggttggttggttggttggt 520
Oy 181 ggggttcgctgcgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 240
    |||||||
Db 521 ggggttcgctgcgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 580
Oy 241 gggcaagccgttaaaccccaactctgaattgttgaacctcgagatagtagaataac 297
    |||||||
Db 581 gggcaagccgttaaaccccaactctgaattgttgaacctcgagatagtagaataac 637

RESULT 4
US-08-905-314-24
: Sequence 24, Application US/08905314
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Novartis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meligs, J. Timothy
: REGISTRATION NUMBER: 38,241
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8587
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 561 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: STRAIN: Fusarium avenaceum
: INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note= "3' end of small subunit"
: OTHER INFORMATION: rRNA gene"
: NAME/KEY: misc_feature
: LOCATION: 31..181
: OTHER INFORMATION: /note= "ITS 1"
: NAME/KEY: misc_feature
: LOCATION: 182..338
: OTHER INFORMATION: /note= "5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature

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: LOCATION: 339..504
: OTHER INFORMATION: /note= "ITS 2"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 505..561
: OTHER INFORMATION: /note= "5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
US-08-905-314-24

Query Match      80.6%; Score 249.8; DB 13; Length 561;
Best Local Similarity 91.6%; Pred. No. 6.3e-71;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

Oy 1 aatgataaagttaagttaagttaagttaagttaagttaagttaagttaagttaagtta 60
    |||||||
Db 232 AATGCGATTAAGTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 291
Oy 61 ttgcgccgcaatattctgcgagcattgaccttcaagcgtcatltaaccctcaagcc 120
    |||||||
Db 292 TTGCGCCCGCTGTGATTTCCGGCGGCGCATGCTTTCGACGCTCATTTCAACCTCAAGCC 351
Oy 121 ccgaggttggttggttggttggttggttggttggttggttggttggttggttggt 179
    |||||||
Db 352 CCCGGGTTGGTGGTGGGATCGGCTGCTTMMGCGCGTCCGCCGCCCAATATACATT 411
Oy 180 ggggttcgctgcgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 239
    |||||||
Db 412 GGGGTCCTGCGTGCACCCCTCATTTGCTAGTAGCTAACACCTCGCAACTGGAACGCGGCG 471
Oy 240 gggcaagccgttaaaccccaactctgaattgttgaacctcgagatagtagaataac 299
    |||||||
Db 472 CGGCCATGCCG-TAAACCCCACTTCTGATTTGACCTCGCATCAGTAGGAATATACC 530
Oy 300 gctgaacttaa 310
    |||||||
Db 531 GCTGAAGTTAA 541

RESULT 5
US-09-423-233-6
: Sequence 6, Application US/09423233
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America as
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE REFERENCE: 03063-0-41MP
: CURRENT APPLICATION NUMBER: US/09/423,233
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 319
: TYPE: DNA
: ORGANISM: Fusarium solani
US-09-423-233-6

Query Match      77.5%; Score 240.2; DB 18; Length 319;
Best Local Similarity 87.4%; Pred. No. 7.4e-68;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

Oy 1 aatgataaagttaagttaagttaagttaagttaagttaagttaagttaagttaagtta 60
    |||||||
Db 3 aatgataaagttaagttaagttaagttaagttaagttaagttaagttaagttaagtta 62
Oy 61 ttgcgccgcaatattctgcgagcattgaccttcaagcgtcatltaaccctcaagcc 120
    |||||||
Db 63 ttgcgccgcaatattctgcgagcattgaccttcaagcgtcatltaaccctcaagcc 122
Oy 121 ccgaggttggttggttggttggttggttggttggttggttggttggttggttggt 173
    |||||||
Db 123 ccgaggttggttggttggttggttggttggttggttggttggttggttggttggt 182

```

OY	174	lclaa tggcgg lctc gctgcagctt cca ttg c tag ag taaa ccct gc caact gt ac	233
	181		
Db	183	tacag tgg cgg tcc ccg ccg cagctt cc tt g g a g a g a c ta aac ctc g caact g aga	242
OY	234	g c g c g c g c c a g c g t t a a a c c c c a a c t c g a t g t g a c c t g a c g t a g a	293
Db	243	g c g c g c g c c a g c g t t a a a c c c c a a c t c g a t g t g a c c t g a c g t a g a	302
OY	294	a t a c c c g t g a a c t t a a	310
Db	303	a t a c c c g t g a a c t t a a	319

```

RESULT      6
US-09-580-797-28
: Sequence 28, Application US/09580797
: GENERAL INFORMATION:
: APPLICANT: Iwen, Peter C.
: APPLICANT: Hinrichs, Steven H.
: APPLICANT: Henry, Travis
: TITLE OF INVENTION: Board of Regents of the University of Nebraska
: TITLE OF INVENTION: Materials and Methods for Molecular
: FILE REFERENCE: UNNC 63149
: CURRENT APPLICATION NUMBER: US/09/580,797
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: fastseq for Windows Version 3.0
: SEQ ID NO 28
: LENGTH: 672
: TYPE: DNA
: ORGANISM: Cylindrocarpum destructans
US-09-580-797-28

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Query Match	64.28;	Score 199;	DB 22;	Length 672;
Best Local Similarity	87.68;	Pred. NO. 3.2e-54;		
Matches 241; Conservative	0;	Mismatches 30;	Indels 4;	Gaps 2

QY	1	aaatcgataaataatgtaattcgtaaatctgaagataacgaatactctgaagcaca	60
Db	360	aaatcgataaataatgtaattcgtaaatctgaagataacgaatactctgaagcaca	419
QY	61	ttgcgcgccgcagatattctgcgcggcagatgcctgtctcgagcgtatcttaaccctcaagcc	120
Db	420	ttgcgcgccgcagatattctgcgcggcagatgcctgtctcgagcgtatcttaaccctcaagcc	479
QY	121	cccgaggttggtggttgggagatcggcaag--cctctggcgcaagccggccccgaattctaat	179
Db	480	cccgaggttggtggttgggagatcggcgctgcgcccccggcgcgccggtctcccaataatga	539
QY	180	ggcggctctcgcgcgcgtcttccatctgcgtatgtagtaaaacccctgcgaactggtatagcgggc	239
Db	540	ggcggctctcgcgcgtatggtcttccctctgcgtatgtagtaaaacccctgcgc---actgtaaaacaagcg	596
QY	240	ggcgcaagccggttaaaacccccaactcttgaatggt	274
Db	597	tggcgaagccggttaaaacccccaactcttgaatggt	631

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RESULT 7
US-09-961-755A-5
: Sequence 5, Application US/09961755A
: GENERAL INFORMATION:
: APPLICANT: Beck, Jim
: APPLICANT: Barnett, Jason
: TITLE OF INVENTION: Detection of Fusarium Species infecting Corn using the
: TITLE OF INVENTION: Polymerase Chain Reaction
: FILE REFERENCE: 60055
: CURRENT APPLICATION NUMBER: US/09/961,755A
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 24

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium subglutinans
US-09-961-755A-5

```

Query Match	62.7%	Score 194.4	DB 36	Length 522
Best Local Similarity	84.3%	Pred. No. 9.5e-53		
Matches 258	Conservative	0	Mismatches 36	Indels 12
			Gaps	3

QY	1	aatcgcataaatgaatggaattgcgaataaataaggaatcatcgaattcttgaacgcaca	60
DB	223	aaatcgcataaatgaatggaattgcgaataaataaggaatcatcgaattcttgaacgcaca	288
QY	61	ttgcgcgccgcgcagtaattctcgcgcgcacatgcctcgtctcgaagcgtcatcttcaaccctcaagcc	120
DB	289	ttgcgcgccgcgcagtaattctcgcgcgcacatgcctcgtctcgaagcgtcatcttcaaccctcaagcc	348
QY	121	ccgcgcgtttgtgtgtcgttgcgcgaatcgcgaagcccttcgcgcgcgaagccgcgcgaatactagtg	180
DB	349	C-----agcttgcgtgtcgttgcgcgaatcgcgcgaatcgcgcgttccccaattgattg	398
QY	181	ggcggtcgcgtgcagcttccattcgtgtgtaataaacccttcgcaactcgtgtacgcgcgc	240
DB	399	ggcggtcgcgtgcagcttccattcgtgtgtaataaacccttcgcaactcgtgtacgtgcgc	457
QY	241	ggcccaagccgtttaaaccccaacttcctgaatgttgaacctgcgaatcaggtagaataatccg	300
DB	458	ggcccaagccgtttaa--cccacaacttcctgaatgttgaacctgcgaatcaggtagaataatccg	516
QY	301	ctgaac	306
DB	517	ctgaac	522

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RESULT      8
US-09-961-755A-8
; Sequence 8, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961.755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Fusarium verticillioides (syn. F. moniliforme)
US-09-961-755A-8

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Query Match	62.7%	Score 194.4	DB 36	Length 522
Best Local Similarity	84.3%	Pred. No. 9.5e-53		
Matches 258	Conservative 0	Mismatches 36	Indels 12	Gaps 3
QY 1	aatgcgaataaataatgataatgcgaataatgaacatcatccttgaacgaca	60		
DB 223	aaatcgaaataaataatgataatgcgaataatgaacatcatccttgaacgaca	288		
QY 61	ttagcgccgcgcgataatctcgcgcggaacatgcctgcttcgaacgcatccaacccaagcc	120		
DB 289	ttagcgccgcgcgataatctcgcgcggaacatgcctgcttcgaacgcatccaacccaagcc	348		
QY 121	cccgagtttgttgttggaatcgcgaagcccttcgcgaacgcgcgcgcgaataatctagtg	180		
DB 349	c-----agcttggtgttgtggaatcgcgaagcccttcgcgaacgcgcgcgcgaataatctagtg	398		

OY 181 gcggtctgcgctgcagctccatctgctagtaaaacccctgcacactgtagcggcgc 240
 ||||| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 399 gcggtcagc-tcgagctccatcagcgtagtaaaacccctgcagctgtagctgc 457
 OY 241 ggcacagccgttaaaccccaactctgaatgttgacctgcagatcaggtlaaggaataccg 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 458 ggcacagccgttaaa-cccacactctgaatgttgacctgcagatcaggtlaaggaataccg 516
 OY 301 ctgaac 306
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 Db 517 ctgaac 522

RESULT 9

US-08-905-314-22
 ; Sequence 22, Application US/08905314
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J.
 ; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
 ; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Novartis Corporation Patent Department
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 20779-2257
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/905,314
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: CGC 1944
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 541-8587
 ; TELEFAX: (919) 541-8589
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 546 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; ORIGINAL SOURCE:
 ; ORGANISM: Fusarium poae
 ; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
 ; IMMEDIATE SOURCE:
 ; CLONE: PCRpoaeT427(1-2), PCRpoaeT534(2-2), and
 ; CLONE: PCRpoaeT756(3-1)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1..30
 ; OTHER INFORMATION: /note="3' end of small subunit"
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 31..180
 ; OTHER INFORMATION: /note="ITS 1"
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 181..337
 ; OTHER INFORMATION: /note="5.8S rRNA gene"
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 338..489
 ; OTHER INFORMATION: /note="ITS 2"

LOCATION: 338..489
 ; OTHER INFORMATION: /note="ITS 2"
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 490..546
 ; OTHER INFORMATION: /note="5' end of large subunit"
 ; OTHER INFORMATION: rRNA gene"
 ; US-08-905-314-22

Query Match 60.5%; Score 187.6; DB 13; Length 546;
 Best Local Similarity 84.5%; Pred. No. 1.6e-50;
 Matches 262; Conservative 0; Mismatches 34; Indels 14; Caps 4;

OY 1 aatgcatagatgtaatgtgaattcgaataatcagtagaatacgaatcttgaacgcaca 60
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 Db 231 AAATGCGATAGTATGTAATGCAGAAATTCAGATGATATCCAAATCTTGAACGCACA 290
 OY 61 ttgcgcccgcagatcttcgcgagcagctgctgtagcgctcatcacaaccccaagcc 120
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 Db 291 TTGCGCCGCCAGTATCTGCGGGCATGCTGTTCCAGCGTCAATTCMAOCCCTCAAGCC 350
 OY 121 ccgagtttggtgttggtggtggtggtggtggtggtggtggtggtggtggtggtggt 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 351 C---AGTTGGTGTGGG-----ATCTGTGCAAAACACAGTCCCAAAATTTGATTG 398
 OY 181 gcggtctgcgctgcagctccatctgctagtagtaaaacccctgcagactgtagcggcgc 240
 ||||| || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 399 GCGGTACG-TCGAGCCTTCATACGTAATTTACACATCGTTACTGTAATCGTCGC 457
 OY 241 ggcacagccgttaaaccccaactctgaatgttgacctgcagatcaggtlaaggaataccg 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 458 GGCACAGCGCGTTAA-CCCACACTTGTGAATGTGACCTCGAGTACAGTACGATACCG 516
 OY 301 ctgaactaa 310
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 Db 517 CTGAACTTAA 526

RESULT 10

US-08-905-314-19
 ; Sequence 19, Application US/08905314
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J.
 ; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
 ; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Novartis Corporation Patent Department
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 20779-2257
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/905,314
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meigs, J. Timothy
 ; REGISTRATION NUMBER: 38,241
 ; REFERENCE/DOCKET NUMBER: CGC 1944
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (919) 541-8587
 ; TELEFAX: (919) 541-8589
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 504 base pairs

```
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium culmorum
INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 1..12
  OTHER INFORMATION: /note= "3' end of small subunit"
  OTHER INFORMATION: rRNA gene"
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 13..161
  OTHER INFORMATION: /note= "ITS 1"
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 162..318
  OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 319..472
  OTHER INFORMATION: /note= "ITS 2"
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 473..504
  OTHER INFORMATION: /note= "5' end of large subunit"
  OTHER INFORMATION: rRNA gene"
US-08-905-314-19
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Query Match 60.2%; Score 186.6; DB 13; Length 504;
Best Local Similarity 82.6%; Pred. No. 3.4e-50;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

```
OY 1 aaatgcgataagtaatgtaattgcaaaatcagtgatcaatcatttgaacgcaca 60
    |||||||
DB 212 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCATCAATCTTGAACGCACA 271
    |||||||
OY 61 ttggccgcgcagatattctgagcgagatgctgttcagagtcattcaaccctaaagc 120
    |||||||
DB 272 TTGCGCCCGCAGATATCTGGCGGGCATGCTGTTGAGCGTCATTCAACCTCAAGCC 331
    |||||||
OY 121 ccggagtttggtgtgaggaatcgcaagcccttcgcaagcccgccgaatctagtg 180
    |||||||
DB 332 C---AGCTTGSTGTTGGG-----AGCTGCACTCCTGCTGCACCTCCCAATACATTG 380
    |||||||
OY 181 ggggtctgcgtcaggttcattgtagtaagaaacccctcgcaactgttacgcgcgc 240
    |||||||
DB 381 GCGGTACGTCGRAGCTTCATAGCGTAGTAATTACATATCGTTACTGTAATCGTGGC 440
    |||||||
OY 241 ggcgaagcgtttaaccaccaactctgtaattgttgacctggaatcagtgatgaataccg 300
    |||||||
DB 441 GGCTACCCCGCTTAAC-CCCAACTTCTGAATGTTGACCTCGATCAGATGAGTAATACCCG 499
    |||||||
OY 301 ctgaa 305
    |||||||
DB 500 CTGAA 504
```

RESULT 11
PCT-US98-25210-4
Sequence 4, Application PC/TUS9825210
GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.
APPLICANT: DESCENZO, Richard A.
APPLICANT: IRELAN, Nancy A.
TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

```
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/25210
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/986,727
FILING DATE: 08-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ekstrom, Richard C.
REGISTRATION NUMBER: 37,027
REFERENCE/DOCKET NUMBER: 009773-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 611 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US98-25210-4
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Query Match 59.7%; Score 185; DB 1; Length 611;
Best Local Similarity 83.1%; Pred. No. 1.2e-49;
Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;

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OY 1 aaatgcgataagtaatgtaattgcaaaatcagtgatcaatcatttgaacgcaca 60
    |||||||
DB 283 AAATGCGATAGTAATGTAATGCAAAATTCAGTGAATCATCATCAATCTTGAACGCACA 342
    |||||||
OY 61 ttggccgcgcagatattctgagcgagatgctgttcagagtcattcaaccctaaagc 120
    |||||||
DB 343 TTGCGCCCGCTGATATCCGAGGGCATGCTGTTGAGCGTCATTCAACCTCAAG-- 400
    |||||||
OY 121 ccggagtttggtgtgaggaatcgcaagcccttcgcaagcccgccgaatctagtg 180
    |||||||
DB 401 -CCTGCTTGTGATGGGCACTGCTCCCGCCCGGAGAGCAGCCCTGAATATCACTG 459
    |||||||
OY 181 ggggtctgcgtcaggttcattgtagtaagaaacccctcgcaactgt--gtacgcgc 238
    |||||||
DB 460 GCGAGCTGCG--CAGGAGCCCGAGCGCAGTAGTAAACCTTCGCGGAGGCCCTGGC 517
    |||||||
OY 239 ggcgcgaagcgtttaaccaccaactctgaaatg--ttgacctcgatcaggtagaataac 297
    |||||||
DB 518 GGTGCCCTGCGCTTAACCCCAACTTCTGAAGATTGACCTCGATCAGGTAGGAATAC 577
    |||||||
OY 298 ccgctgaactaa 310
    |||||||
DB 578 CCGCTGAACCTTAA 590
```

RESULT 12
US-08-905-314-21
Sequence 21, Application US/08905314
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novartis Corporation Patent Department

```

1 RESULT 13
2 US-08-905-314-20
3 Sequence 20, Application US/08905314
4 GENERAL INFORMATION:
5 APPLICANT: Beck, James J.
6 TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
7 TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
8 NUMBER OF SEQUENCES: 24
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Novartis Corporation Patent Department
11 STREET: 3054 Cornwallis Road
12 CITY: Research Triangle Park
13 STATE: NC
14 COUNTRY: USA
15 ZIP: 20779-2257
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/905,314
23 FILING DATE:
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Melgs, J. Timothy
27 REGISTRATION NUMBER: 38,241
28 REFERENCE/DOCKET NUMBER: CGC 1944
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (919) 541-8587
31 TELEFAX: (919) 541-8689
32 INFORMATION FOR SEQ ID NO: 20:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 503 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: DNA (genomic)
39 ORIGINAL SOURCE:
40 ORGANISM: Fusarium graminearum
41 INDIVIDUAL ISOLATE: R-8417, and R-8546
42 INDIVIDUAL ISOLATE: (consensus sequence)
43 FEATURE:
44 NAME/KEY: misc_feature
45 LOCATION: 1..9
46 OTHER INFORMATION: /note="3' end of small subunit
47 OTHER INFORMATION: rRNA gene"
48 FEATURE:
49 NAME/KEY: misc_feature
50 LOCATION: 10..155
51 OTHER INFORMATION: /note="ITS 1"
52 FEATURE:
53 NAME/KEY: misc_feature
54 LOCATION: 156..312
55 OTHER INFORMATION: /note="5.8S rRNA gene"
56 FEATURE:
57 NAME/KEY: misc_feature
58 LOCATION: 313..466
59 OTHER INFORMATION: /note="ITS 2"

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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 467..503
; OTHER INFORMATION: /note="5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
US-08-905-314-20
```

```
Query Match 58.2%; Score 180.4; DB 13; Length 503;
Best Local Similarity 80.0%; Pred. No. 3.7e-48;
Matches 248; Conservative 12; Mismatches 38; Indels 12; Gaps 4;
```

```
QY 1 aatgcgataagtaatgtaattgcaaaatcagtcgaatcatcgaatccttgaagcaca 60
DB 206 AATGCGATAGTAATGTAATGCAAGATTGATGATCAATCAACGAACTTTGAAGCGCWSA 265
QY 61 ttgcccgcagcagatctctggcgagcagcctgttcgaagcgtcatctcaaccctcaagcc 120
DB 266 TTGCKMCKRCAGTATTTGGCGGCATGCTGTGACGCGTCAATTTCAACCTCAAGCC 325
QY 121 cccgggttggtgttggtggagtcggcaagcccttgcggaagcccgcccgaaatctagt 180
DB 326 C---ACVTTGGTGTGGGAGRTGCAKCC-----TTRTKACCTCCCAATAARTTG 375
QY 181 ggcgtctgcgtcagccttcacatctgctagtaaaacccctcgcaactgtacgcggcgcc 240
DB 376 GCGGTCAAG-TCGAAGCTTCATAGCGTACTAGTACACATGCTTACTGCTATGCTGCC 434
QY 241 ggcgaagccggttaaaccccccaactctctgaatgttgactcgtgaatgaagtaaccgc 300
DB 435 GGTCTACGCGGTTAA-CCCCAAGCTTGTGAATGTGACCTCGGATCAGTAGAATACCCG 493
QY 301 ctgaactaa 310
DB 494 CTGAAGCTAA 503
```

```
RESULT 14
US-09-961-755A-6
; Sequence 6, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Beck, Jim
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: Polymerase Chain Reaction
; CURRENT APPLICATION NUMBER: US/09/961,755A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Gibberella zeae
US-09-961-755A-6
```

```
Query Match 57.8%; Score 179.2; DB 36; Length 521;
Best Local Similarity 83.3%; Pred. No. 9.2e-48;
Matches 255; Conservative 0; Mismatches 38; Indels 13; Gaps 4;
```

```
QY 1 aatgcgataagtaatgtaattgcaaaatcagtcgaatcatcgaatccttgaagcaca 60
DB 229 AATGCGATAGTAATGTAATGCAAGATTGATGATCAATCAACGAACTTTGAAGCGCWSA 288
QY 61 ttgcccgcagcagatctctggcgagcagcctgttcgaagcgtcatctcaaccctcaagcc 120
DB 289 ttgcccgcagcagatctctggcgagcagcctgttcgaagcgtcatctcaaccctcaagcc 348
QY 121 cccgggttggtgttggtggagtcggcaagcccttgcggaagcccgcccgaaatctagt 180
DB 349 C---agcttggtgttggtg-----agctgcagtcctctgctgactccccaataacatg 397
```

```
QY 181 ggcgtctgcgtcagccttcacatctgctagtaaaacccctcgcaactgtacgcggcgcc 240
DB 398 ggcgtcagc-tcgaagcttcacatctgctagtaaaacccctcgcaactgtacgcggcgcc 456
QY 241 ggcgaagccggttaaaccccccaactctctgaatgttgactcgtgaatgaagtaaccgc 300
DB 457 ggcgaagccggttaaa-cccccaactctctgaatgttgactcgtgaatgaagtaaccgc 515
QY 301 ctgaac 306
DB 516 ctgaac 521
```

```
RESULT 15
US-09-580-797-11
; Sequence 11, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; TITLE OF INVENTION: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-580-797-11
```

```
Query Match 57.4%; Score 177.8; DB 22; Length 620;
Best Local Similarity 84.5%; Pred. No. 2.8e-47;
Matches 251; Conservative 0; Mismatches 32; Indels 14; Gaps 4;
```

```
QY 1 aatgcgataagtaatgtaattgcaaaatcagtcgaatcatcgaatccttgaagcaca 60
DB 338 AATGCGATAGTAATGTAATGCAAGATTGATGATCAATCAACGAACTTTGAAGCGCWSA 397
QY 61 ttgcccgcagcagatctctggcgagcagcctgttcgaagcgtcatctcaaccctcaagcc 120
DB 398 ttgcccgcagcagatctctggcgagcagcctgttcgaagcgtcatctcaaccctcaagcc 457
QY 121 cccgggttggtgttggtggagtcggcaagcccttgcggaagcccgcccgaaatctagt 180
DB 458 C---agcttggtgttggtg-----cgtaactgcgtccccaatctagt 505
QY 181 ggcgtctgcgtcagccttcacatctgctagtaaaacccctcgcaactgtacgcggcgcc 240
DB 506 ggcgtcagc-tcgaagcttcacatctgctagtaaaacccctcgtaactgtacgcggcgcc 564
QY 241 ggcgaagccggttaaaccccccaactctctgaatgttgactcgtgaatgaagtaaccgc 297
DB 565 ggcgaagccggttaa-cccccaactctctgaatgttgactcgtgaatgaagtaaccgc 620
```

```
Search completed: August 22, 2002, 00:39:29
Job time: 13054 sec
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Accession	Sequence	Position
Db	181 gggggtctgcgcgtgcagcttcacattgcgtgtagtaaaacccctgcacatctgtagcgcgcc	240
Oy	241 gggcgaagccgtttaaaccccccaactctcgaattgttgacctcgatcagtgtagaataaccg	300
Db	241 gggcgaagccgtttaaaccccccaactctcgaattgttgacctcgatcagtgtagaataaccg	300
Oy	301 ctgaacttaa 310	
Db	301 ctgaacttaa 310	

```

: RESULT 2
: US-10-046-955-6
: Sequence 6, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046, 955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423, 233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: SeqEdit Ver. 2.0
: SEQ ID NO 6
: LENGTH: 319
: TYPE: DNA
: ORGANISM: Fusarium solani
: US-10-046-955-6

```

[illegible]

```

PCT-US02-11769-2
: Sequence 2, Application PC/TUS0211769
: GENERAL INFORMATION:
: APPLICANT: Strobel, Gary
: APPLICANT: Manker, Denise
: TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
: TITLE OF INVENTION: USE
: FILE REFERENCE: AO 2019, 40
: CURRENT APPLICATION NUMBER: PCT/US02/11769
: CURRENT FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 60/283,902
: PRIOR FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: 60/363,072
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 652
: TYPE: DNA
: ORGANISM: Muscador albus
PCT-US02-11769-2

```

Query Match	43.98	Score 136.2	DB 1	Length 652
Best Local Similarity	71.78	Pred. No. 3.8e-35		
Matches 223	Conservative 0	Mismatches 78	Indels 10	Gaps 3
Qy	1	aatcgatagaatgaatgtgaattgcgaatctaaatctaaagaaatctgaatcttgaacgcaca	60	
Db	329	aatcgatagaatgaatgtgaattgcgaatctaaagaaatctgaatcttgaacgcaca	368	
Qy	61	ttgcgcgcgcgaatattctgcgcgcgaatctgcgttcgcgcgcgttcattcaaccctcaagcc	120	
Db	389	ttgcgcgcgcgaatattctgcgcgcgaatctgcgttcgcgcgcgttcattcaaccctcaagcc	448	
Qy	121	ccgcggttggtgtttggggatcgcgaagcccttcgcgcgaagccgcgcgcgcgaatctgatt	180	
Db	449	ctgttgcttgatgcgttgggaagcc----taaggcacttcgcgttagctccctcaaatgtgtg	503	
Qy	181	gcgcgttcgcgttcgaagcttcgatctgtagtaagaaacccgcgaact-gttagcgcgcgc	239	
Db	504	gcgcgagtgtgtc-----taactctaggcgtgaataaatctatctgcgtctgtgtgtgttc	559	
Qy	240	cgagcgaagccgtttaaaccctcccaactcttgaatgtttgacctcgatcagtaggaataacc	299	
Db	560	cgagccctgcgtttaaaccctccctataataaagttgtaactcgtatcagtaggaataacc	619	
Qy	300	gctgaacttaa 310		
Db	620	gctgaacttaa 630		

RESULT 4
US-10-046-955-3
Sequence 3, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400

[illegible]

```

RESULT 7
US-09-766-173C-4
: Sequence 4: Application US/09766173C
:
: GENERAL INFORMATION:
: APPLICANT: Carroll, George C.
: TITLE OF INVENTION: Materials and Methods For Detection of
: Patogenic Guinardia Citricarpa
: FILE REFERENCE: Oregon 99-09
: CURRENT APPLICATION NUMBER: US/09/766,173C
: CURRENT FILING DATE: 2001-01-22
: PRIOR APPLICATION NUMBER: PCT/US01/01735
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/177,013
: PRIOR FILING DATE: 2000-01-19
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 641
:
: TYPE: DNA
: ORGANISM: Guinardia Citricarpa
: US-09-766-173C-4

```

Query Match	40.28;	Score 124.6;	DB 5;	Length 641;
Best Local Similarity	64.68;	Pred. No. 2.8e-31;		
Matches 201; Conservative	0;	Mismatches 109;	Indels 1;	Gaps 1

OY	1	aaatgcataaagtaattgtaattgcgaanaattcagtaatacatcgaattctttgaacgaca	60
Db	318	aaatgcataaagtaattgtaattgcgaanaattcagtaatacatcgaattctttgaacgaca	377
OY	61	ctgcgcgccgaagtaatctcggcggaagtcgcgtctcgagcgatcattcaacctcaagcc	120
Db	378	ctgcgcgcccttgatcatccggcggaagtcgcgtctcgagcgatcattcaacctcaagct	437
OY	121	cccgagctcttgctcttgaggatctgcgcaagacctctgcggcaagcccgagcc-cggaattagt	179
Db	438	ctgcgttgtaattcggcgagctccgcgcggcggaagccctcggaagacctcggcgagcggt	497
OY	180	ggcgctctgcctgcgaagcttcacatctgcgtagtagtaaaacctgcgaactcgtgaacgcggcg	239
Db	498	ctcgcgctcagagcgttagtagtaaaataatctcgctcttgaggaaggcgctcgccgcg	557
OY	240	cggcgaagcgcgttaaaaccccccaactctgaattctagacctcggaataagtaggaataacc	299
Db	558	gacacatgcgaactcgcgtacataattttccaaagtgtaactcgtgatacaggtaaagataacc	617
OY	300	gctgaacttaa 310	
Db	618	gctgaacttaa 628	

```

RESULT      8
US-09-517-790--5
; Sequence 5, Application US/09517790
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F
; TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of F
; TITLE OF INVENTION: Diseases in plants
; FILE REFERENCE: RU-0093

```

```

? CURRENT APPLICATION NUMBER: US-09/517,790
? CURRENT FILING DATE: 2000-03-02
? PRIOR APPLICATION NUMBER: US 60/123,099
? PRIOR FILING DATE: 1999-03-05
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 5
? LENGTH: 536
? TYPE: DNA
? ORGANISM: Amapelomyces humuli
US-09-517-790-5

```

Query Match	40.1%;	Score 124.4;	DB 5;	Length 536;
Best Local Similarity	69.4%;	Pred. No. 3e-31;		
Matches 215; Conservative	0;	Mismatches 86;	Indels 9;	Gaps 3;

QY	1	aaatgcgataagtaatgtaattgcacaatctcagtgatactcgaattcttgaagcaca	60
Db	220	aaatgcgataagtaagtgatgtaattgcagaatctcagtgatactcgaattcttgaagcaca	279
QY	61	ttgcgcgccgcagatattcttcgcgagcatgcctgtctcagcgatcaattcaacctcaagcc	120
Db	280	ttgcgcgccctctgtaattccatcgaggcactgcctgtctcagcgatcaattcttgaacctcaag--	337
QY	121	cccgagatttggttgtcttgaggatcgcgaagcccttcgcgcaagccgcgcccgaaatctaatg	180
Db	338	ctctcgcttggtggtgtgtgttcttcgcctctcgcgtgtgtaattcgcctcaaacaaattg	397
QY	181	ggcgtcttcgcgtcagcgtcttccattgctgtagtaataaacctcgcgaactggtlaacgcgcgc	240
Db	398	gcacgcgcgcgcatgtaatttcggaagcgcagct----acatctcgcgccttgcacatcaaac	452
QY	241	ggccaaagccgttaaacccccaactctcgaattgttgaactcgcgatacagtgagataaccg	300
Db	453	gacgacgtc--caaaagtaactcttttaactactcttgactcgcgatacagtgatggataaccg	510
QY	301	ctgaacttaa	310
Db	511	ctgaacttaa	520

```

RESULT      9
PCT-US02-11769-4
Sequence 4, Application PC/TUS0211769
GENERAL INFORMATION:
APPLICANT: Strobel, Gary
APPLICANT: Manke, Denise
TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: AQ 2019.40
CURRENT APPLICATION NUMBER: PCT/US02/11769
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/283,902
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: 60/363,072
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 650
TYPE: DNA
ORGANISM: Muscodor roseus
PCT-US02-11769-4

```

	40.1%	Score 124.2	DB 1,	length 650;
Query Match	Similarity 71.4%	Pred. No.	3,8e-31;	
Best Local		Matches 222;	Conservative 0;	Mismatches 78; Indels 11; Gaps 4;
Dy	1	aatgagcaaaagtgaatgcgaattcagaataacatcgatcgttccttgaacgaca	60	
Db	329	aatggagaaaagtgaatgcgaattcagaataacatcgatcgttccttgaacgaca	388	

[illegible]

RESULT 10
US-10-046-955-5
Sequence 5, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Liliانا
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
TITLE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046, 955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423, 233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 365
TYPE: DNA
ORGANISM: Aspergillus nidulans
US-10-046-955-5

Query Match	39.78;	Score 123.2;	DB 7;	Length 365;
Best Local Similarity	66.58;	Pred. No. 6.8e-31;		
Matches 210; Conservative	0;	Mismatches 98;	Indels 8;	Gaps 2

[illegible]

Accession	Sequence	Length
OY	cggcgcgcgcacagcgcgtttaaaccgccactctctgaagtgtgactcgtgacagtagtagaa	254
db	gagcgcgcgcgcgcgtctcccaactctcttctcaggtctgaccctcgacatgagttagga	349
OY	taccgcgtcgaacttaa	310
db	taccgcgtcgaacttaa	365

```

RESULT 11
; Sequence 5, Application US/09/766/173C-5
; GENERAL INFORMATION:
; APPLICANT: Carroll, George C.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Pathogenic Guinardia Citricarpa
; FILE REFERENCE: Oregon 99-09
; CURRENT APPLICATION NUMBER: US/09/766,173C
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/01735
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/177,013
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Guinardia Citricarpa
US-09-766-173C-5

```

Query Match	38.8%	Score 120.2	DB 5	Length 618
Best Local Similarity	66.5%	Pred. NO. 7.9e-30		
Matches 208; Conservative	0	Mismatches 93	Indels 12	Gaps 2

Oy	1	aaatgcatgaatgatactgaaatctgcaaaatcagtagaatacgcgaatcctttgaaacgaca	60
Db	313	aaatgcatgaatgaatgatactgaaatcagtagaatacgcgaatcctttgaaacgaca	372
Oy	61	ttgcgccccgcagatattctgcgcggagcagtcctgtttcagcgtcaattccaacccccaagcc	120
Db	373	ttgcgccccgcagatattctgcgcggagcagtcctgtttcagcgtcaattccaacccccaagct	432
Oy	121	ccgcggtttgtgtttggtggaatcagccaagccctttgcgcgaagccgcgcgcgaatactcgtg	180
Db	433	ctgctctgtatcttgagcaagctccgcctgcgcgagcgtgccttgaaagctcg-----gcg	485
Oy	181	gcggtctcgcgtcgcagcttccattgcgttagtagtaaaaacccctgcgaacattggtacgcgcg-	239
Db	486	acgcggtctcgcgtcgcagcgttagtagtaaaaatctcgccttgcgtgagtgctgcgcgcgcg	545
Oy	240	----gcgcgaagcgcgttaaaccccccaactttgaaatttgaaacctcggaatcaagtaggaat	295
Db	546	ccgcgcgcgaatcgaaccttcgctgccttattttcccaaggttgaaacctcggaatcagaatgagat	605
Oy	296	accgcgtgaactt 308	
Db	606	accgcgtgaactt 618	

RESULT 12
US-10-046-955-27
; Sequence 27, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

```
; TITLE OF INVENTION: Other Filamentous Fungi
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO: 27
; LENGTH: 343
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-27
```

```
Query Match      36.0%; Score 111.6; DB 7; Length 343;
Best Local Similarity 79.5%; Pred. No. 4.9e-27;
Matches 132; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
```

```
Oy 1 aatgcgataaagtgaattgcgaataatcagtcgaatcatcgaatcttgaacgcaca 60
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 aatgcgataaagtgaattgcgaataatcagtcgaatcatcgaatcttgaacgcaca 60

Oy 61 ttgcgcgccgcaatcttcggggcgagcagccctgttcgagcgtcatcttaaccctaacgc 120
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ttgcgcgccgcaatcttcggggcgagcagccctgttcgagcgtcatcttaaccctaacgc 120

Oy 121 cccgggttctgttggggtatcggcaagcccttcgcgcaagccgcgcgc 166
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 tccgttctccagggaaagctcagggctggttggggcgctaacgcgc 166
```

```
RESULT 13
US-10-046-955-26
; Sequence 26, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO: 26
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
US-10-046-955-26
```

```
Query Match      36.0%; Score 111.6; DB 7; Length 344;
Best Local Similarity 79.5%; Pred. No. 4.9e-27;
Matches 132; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Oy 1 aatgcgataaagtgaattgcgaataatcagtcgaatcatcgaatcttgaacgcaca 60
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 2 aatgcgataaagtgaattgcgaataatcagtcgaatcatcgaatcttgaacgcaca 61

Oy 61 ttgcgcgccgcaatcttcggggcgagcagccctgttcgagcgtcatcttaaccctaacgc 120
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 ttgcgcgccgcaatcttcggggcgagcagccctgttcgagcgtcatcttaaccctaacgc 121

Oy 121 cccgggttctgttggggtatcggcaagcccttcgcgcaagccgcgcgc 166
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 tccgttctccagggaaagctcagggctggttggggcgctaacgcgc 167
```

```
RESULT 14
US-10-046-955-29
; Sequence 29, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO: 29
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Sporothrix schenckii
US-10-046-955-29
```

```
Query Match      35.1%; Score 108.8; DB 7; Length 336;
Best Local Similarity 72.6%; Pred. No. 4.1e-26;
Matches 154; Conservative 0; Mismatches 57; Indels 1; Gaps 1;
```

```
Oy 11 agtaatgtgaattgcgaataatcagtcgaatcatcgaatcttgaacgcacatcgcgcgc 70
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 actaatgtgaattgcgaataatcagtcgaatcatcgaatcttgaacgcacatcgcgcgc 70

Oy 71 cagatcttcggcgagcagctgttcgagcgtcatcttaaccctaacgcccgggttcg 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 cagatcttcggcgagcagctgttcgagcgtcatcttaaccctaacgcccgggttcg 130

Oy 131 gtgttggtatcggcaagc-ccttcgcgcaagccgcccgaataatagtgcgtctcg 189
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131 cgtcgtgttcggcgccctcccttcgcgggggcccccgaagaagcagtggtgggcccct 190

Oy 190 ctgcaagcttcagtcgtagttaaaacct 221
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 gtggaagcttcgagcagatcagcaagcat 222
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 15
US-10-046-955-25
; Sequence 25, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
```

```

:   APPLICATOR: Choi, Jong Soo
:   TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
:   TITLE OF INVENTION: Other Filamentous Fungi
:   FILE REFERENCE: 6395-62064
:   CURRENT APPLICATION NUMBER: US/10/046,955
:   PRIOR APPLICATION NUMBER: 2002-06-04
:   PRIOR FILING DATE: 2000-06-27
:   PRIOR APPLICATION NUMBER: PCT/US98/08926
:   PRIOR FILING DATE: 1998-05-01
:   PRIOR APPLICATION NUMBER: US 60/045,400
:   PRIOR FILING DATE: 1997-05-02
:   NUMBER OF SEQ ID NOS: 61
:   SOFTWARE: PatentIn Ver. 2.0
:   SEQ ID NO 25
:   LENGTH: 346
:   TYPE: DNA
:   ORGANISM: Pseudallescheria boydii
:   US-10-046-955-25

```

Query Match	34.8%;	Score 107.8;	DB 7;	Length 346;
Best Local Similarity	70.4%;	Pred. No. 9e-26;		
Matches 243;	Conservative 0;	Mismatches 67;	Indels 35;	Gaps 6;

Oy	1	aaatgcgaataagtaatgtaattgcgaataatcaatgaatcatcgaatcttg-aaocgac	59
Oy	2	aaatgcgaataagtaatgtaattgcgaataatcaatgaatcatcgaatcttg-aaocgac	61
Oy	60	attgcgcgcgcgaatlatcttgcgcgcgcgaatctgtcttcgaagcgtcaattcaacctcaagc	119
Db	62	attgcgcgcgcgaatlatcttgcgcgcgcgaatctgtcttcgaagcgtcaattcaacctcaagc	121
Oy	120	ccccc-----gatttgtgtttgggagtcgcgcaaaccccttgcgcaag	161
Db	122	cttcgattccctcaggaagctcgaagtcgtgtgtgtgggcgtcaagcaagttcttcgaac	181
Oy	162	cc-----ggccgcgaaatcattagtgcggtctcgcgcgcagcttccat-tgcgtagtatgta	214
Db	182	ctctcgcagtcgcctgcgaataacagctgcggtccgcgcgcgcgttgcctctcgtatagaagtc	241
Oy	215	aaaccc-----gcaacttgttaacgcgcgcgcgcgaagcgcgttaaaccccaacttga	269
Db	242	tcttttgcaagctgcgcatgtgtgtccgcgcgcgcgcgcgttcgaaccactactaactcc	301
Oy	270	a-----tgttgacctgcgatacagctagaatacccgctgaactta	310
Db	302	aaatgttgacctgcgatacagctagaagttatcccgctgaactta	346

Search completed: August 22, 2002, 00:50:50
Job time: 11890 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:49 : Search time 2238.68 Seconds
(without alignments)
168.259 Million cell updates/sec

Title: us-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtgcggtctcgct 18

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
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27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
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	1	16.4	91.1	310	8	AF117922	AF117922 Gibberella
	2	16.4	91.1	351	8	AF162903	AF162903 Fusarium
	3	16.4	91.1	419	8	AF111060	AF111060 Fusarium
	4	16.4	91.1	457	8	AF261745	AF261745 Cylindroc
	5	16.4	91.1	458	8	AF008562	AF008562 Fusarium
	6	16.4	91.1	464	8	AF261740	AF261740 Calonectr
	7	16.4	91.1	466	8	AF261740	AF261740 Calonectr
	8	16.4	91.1	466	8	NGA228662	AJ228662 Nectria g
	9	16.4	91.1	466	8	NGA228663	AJ228663 Nectria g
	10	16.4	91.1	466	8	NGA228664	AJ228664 Nectria g
	11	16.4	91.1	466	8	NGA228665	AJ228665 Nectria g
	12	16.4	91.1	466	8	NGA228666	AJ228666 Nectria g
	13	16.4	91.1	466	8	NGA228667	AJ228667 Nectria g
	14	16.4	91.1	466	8	NGA228668	AJ228668 Nectria g
	15	16.4	91.1	466	8	NGA228669	AJ228669 Nectria g
	16	16.4	91.1	466	8	NGA228670	AJ228670 Nectria g
	17	16.4	91.1	466	8	NGA228671	AJ228671 Nectria g
	18	16.4	91.1	466	8	NGA228672	AJ228672 Nectria g
	19	16.4	91.1	466	8	NGA228673	AJ228673 Nectria g
	20	16.4	91.1	466	8	NGA228674	AJ228674 Nectria g
	21	16.4	91.1	466	8	NGA228675	AJ228675 Nectria g
	22	16.4	91.1	466	8	NGA228676	AJ228676 Nectria g
	23	16.4	91.1	466	8	NGA228677	AJ228677 Nectria g
	24	16.4	91.1	466	8	NGA228678	AJ228678 Nectria g
	25	16.4	91.1	466	8	NGA228679	AJ228679 Nectria g
	26	16.4	91.1	466	8	NGA228680	AJ228680 Nectria g
	27	16.4	91.1	466	8	NGA228681	AJ228681 Nectria g
	28	16.4	91.1	466	8	NGA228682	AJ228682 Nectria g
	29	16.4	91.1	466	8	NGA228683	AJ228683 Nectria g
	30	16.4	91.1	466	8	NGA228684	AJ228684 Nectria g
	31	16.4	91.1	466	8	NGA228685	AJ228685 Nectria g
	32	16.4	91.1	466	8	NGA228686	AJ228686 Nectria g
	33	16.4	91.1	466	8	NGA228687	AJ228687 Nectria g
	34	16.4	91.1	466	8	NGA228688	AJ228688 Nectria g
	35	16.4	91.1	466	8	NGA228689	AJ228689 Nectria g
	36	16.4	91.1	466	8	NGA228690	AJ228690 Nectria g
	37	16.4	91.1	466	8	NGA228691	AJ228691 Nectria g
	38	16.4	91.1	466	8	NGA228692	AJ228692 Nectria g
	39	16.4	91.1	469	8	NGA228693	AJ228693 Nectria g
	40	16.4	91.1	470	8	NRA7353	AJ007353 Nectria r
	41	16.4	91.1	470	8	AF132800	AF132800 Fusarium
	42	16.4	91.1	470	8	AF440528	AF440528 Fusarium
	43	16.4	91.1	470	8	AF440530	AF440530 Fusarium
	44	16.4	91.1	470	8	AF440533	AF440533 Fusarium
	45	16.4	91.1	471	8	AF440551	AF440551 Fusarium
						AF150468	Nectria h

ALIGNMENTS

RESULT 1
AF117922 310 bp DNA linear PLN 17-JUN-2000
LOCUS Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial
DEFINITION Sequence: Internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.

ACCESSION AF117922
VERSION AF117922
KEYWORDS AF117922.1 GI:8570108

SOURCE
ORGANISM
Gibberella fujikuroi.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.

REFERENCE
AUTHORS Choi, J.S., Westernman, J.M. and Morrison, C.J.

TITLE Rapid differentiation of filamentous fungi using species-specific
DNA probes

JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE 2 (bases 1 to 310)

AUTHORS Choi, J.S., Westernman, J.M. and Morrison, C.J.

TITLE Direct Submission
JOURNAL Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

FEATURES
source Location/Qualifiers
1..310
/organism="Gibberella fujikuroi"
/strain="ATCC 38519"
/db_xref="ATCC:38519"
/db_xref="taxon:5127"
<1..159
/product="5.8S ribosomal RNA"
159..272
/note="ITS2"
/product="internal transcribed spacer 2"
273..>310
/product="28S ribosomal RNA"
BASE COUNT 73 a 86 c 80 g 71 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 310;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctatgacggtctcgct 18
||||| |||||||
Db 174 TCTAGTGGCGCTCTCGCT 191

RESULT 2
AF162903 351 bp DNA linear PLN 04-AUG-1999
LOCUS
DEFINITION Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence;
internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence.
ACCESSION AF162903
VERSION AF162903.1 GI:5690392
KEYWORDS
SOURCE
ORGANISM
Fusarium proliferatum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
REFERENCE
AUTHORS Min,B.R.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong No-gu, Seoul 110-743, Korea
Location/Qualifiers
1..351
/organism="Fusarium proliferatum"
/strain="6787"
/db_xref="taxon:42674"
<1..128
/product="5.8S ribosomal RNA"
129..293
/product="internal transcribed spacer 2"
294..>351
/product="28S ribosomal RNA"
BASE COUNT 87 a 94 c 94 g 76 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 351;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctatgacggtctcgct 18
||||| |||||||
Db 195 TCTACTGGCGCTCTCGCT 212

RESULT 3
AF111060 419 bp DNA linear PLN 20-JAN-1999
LOCUS
DEFINITION Fusarium subglutunum var. subglutunum strain BBA62431 internal
transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,

complete sequence; and internal transcribed spacer 2, partial
sequence.
AF111060 GI:4160484
ACCESSION
VERSION AF111060.1
KEYWORDS
SOURCE
ORGANISM
Fusarium subglutunum var. subglutunum.
Fusarium subglutunum var. subglutunum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE
AUTHORS Bulat,S.A., Yli-Mattila,T. and Alekhina,I.A.
TITLE Molecular taxonomy of Fusarium strains by means of ribotyping, rDNA
sequencing and up-PCR analysis. A case study of Sporotrichiella
section
Unpublished
2 (bases 1 to 419)
Bulat,S.A. and Alekhina,I.A.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1998) Department of Molecular and Radiation
Biophysics, Petersburg Nuclear Physics Institute RAS, Gatchina,
Leningrad Region 188350, Russia
Location/Qualifiers
1..419
/organism="Fusarium subglutunum var. subglutunum"
/strain="BBA62431"
/variety="subglutunum"
/db_xref="taxon:86548"
<1..136
/note="ITS1"
/product="internal transcribed spacer 1"
137..294
/product="5.8S ribosomal RNA"
295..>419
/note="ITS2"
/product="internal transcribed spacer 2"
BASE COUNT 105 a 118 c 98 g 98 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 419;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctatgacggtctcgct 18
||||| |||||||
Db 365 TCTAGTGGCGCTCTCGCT 382

RESULT 4
AF261745 457 bp DNA linear PLN 26-SEP-2000
LOCUS
DEFINITION Cylindrocylindrella parva internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
AF261745
VERSION AF261745.1 GI:10304122
KEYWORDS
SOURCE
ORGANISM
Cylindrocylindrella parva.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Cylindrocylindrella.
REFERENCE
AUTHORS Risede,J.-M. and Simoneau,P.
TITLE Typing Cylindrocylindrium species by analysis of ribosomal DNA spacers
polymorphism: application to field isolates issued from banana
rhizosphere
Unpublished
2 (bases 1 to 457)
Risede,J.-M. and Simoneau,P.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (28-APR-2000) Plant Pathology, Universite d'Angers, 2 Bd
Lavoisier, Angers 49045, France
Location/Qualifiers

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source              1. .457
                    /organism="Cylindrocapsa parva"
                    /strain="MUCL 636"
                    /db_xref="taxon:137496"
misc_RNA            1. .128
                    /product="Internal transcribed spacer 1"
rRNA                129. .296
                    /product="5.8S ribosomal RNA"
misc_RNA            297. .457
                    /product="Internal transcribed spacer 2"
BASE COUNT          101 a      133 c      109 g      114 t
ORIGIN
Query Match          91.1%; Score 16.4; DB 8; Length 457;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 tctagtacggtctgcgt 18
        ||||||| |||||||||
Db      366 TCTATGCGGCGTCTGCCT 383

```

RESULT	5
AF008562	
LOCUS	
DEFINITION	AF008562 458 bp DNA linear PLN 07-JUN-1999 Fusarium redolens internal transcribed spacer 1, partial sequence, 5.8S ribosomal RNA gene, complete sequence, and internal transcribed spacer 2, partial sequence.
ACCESSION	AF008562
VERSION	AF008562.1 GI:4102047
KEYWORDS	.
SOURCE	Fusarium redolens. Fusarium redolens
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; microsporic Hypocreales; Fusarium.
REFERENCE	1 (bases 1 to 458) Paavainen-Huhtala,S., Hyvonen,J., Bulat,S.A. and Yli-Mattila,T. RAPD-PCR, isozyme, rDNA RFLP and rDNA sequence analyses in identification of Finnish Fusarium oxysporum isolates <i>Mycol. Res.</i> 103 (5), 625-634 (1999)
JOURNAL,	2 (bases 1 to 458) Yli-Mattila,T., Paavainen-Huhtala,S. and Hyvonen,J. Direct Submissions Submitted (16-JUN-1997) Lab. of Plant Physiology and Molecular Biology, Dept. of Biology, Univ. of Turku, Turku 20014, Finland
AUTHORS	I. .458
TITLE	
JOURNAL,	
FEATURES	
SOURCE	

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misc_RNA
rRNA
misc_RNA
BASE COUNT      115 a      130 c      106 g      104 t      3 others
ORIGIN

Query Match          91.1%; Score 16.4; DB 8; Length 458;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 tctagtgaaggtctcgct 18
          ||||| |||||
Db      360 TCTAGTGCGCCTCTCGCT 377

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AF261740	464 bp	DNA	linear	PLN 26-SEP-2000
LOCUS				
DEFINITION	Calonectria kyotensis strain ATCC22677 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.			
ACCESSION	AF261740			
VERSION	AF261740.1			
KEYWORDS	GI:10304117			
SOURCE	.			
ORGANISM	Calonectria kyotensis. Calonectria kyotensis Eutariota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hyphocrea; Nectriaceae; Calonectria.			
REFERENCE	1 (bases 1 to 464)			
AUTHORS	Risede, J.-M. and Simoneau, P.			
TITLE	Typing <i>Cylindrocylindrium</i> species by analysis of ribosomal DNA spacers polymorphism: application to field isolates issued from banana rhizosphere			
JOURNAL	unpublished			
REFERENCE	2 (bases 1 to 464)			
AUTHORS	Risede, J.-M. and Simoneau, P.			
TITLE	Direct Submission			
JOURNAL	Submitted (28-APR-2000) Plant Pathology, Universite d'Angers, 2 Bd Lavoisier, Angers 49045, France			
FEATURES	location/Qualifiers			
Source	1..464			

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misc_RNA
/rnaism="Calonectella kyotensis"
/strain="ATCC22677"
/db_xref="ATCC:22677"
/db_xref="taxon:40623"
1..128
/product="internal transcribed spacer 1"
129..297
/product="5.8S ribosomal RNA"
298..464
/product="internal transcribed spacer 2"

BASE COUNT      110 a      132 c      107 g      115 t
ORIGIN

Query Match      91.1%; Score 16.4; DB 8; Length 464;
Best Local Similarity 94.4%; Pred. NO. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 tctatgacggtctgcgt 18
||||| |||||||
Db      371 tctatgacggtctgcgt 388

```

RESULT	7
LOCUS	NGA228662
DEFINITION	Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA gene, and internal transcribed spacer 2 (ITS 2) (isolate CBS 100318).
ACCESSION	AJ228662
VERSION	AJ228662.1 GI:4210757
KEYWORDS	18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer; ITS1; ITS2.
SOURCE	Neonectria galligena.
'ORGANISM	Neonectria galligena
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neonectria.
AUTHORS	1 (bases 1 to 466)
TITLE	Langreil, S.R.H.
JOURNAL	Direct Submission
REFERENCE	Submitted (07-APR-1998) Langreil, S.R.H., Department of Biological Sciences, Wye College, University of London, Wye, Ashford, Kent., TN25 5AH, UNITED KINGDOM
AUTHORS	2 (bases 1 to 466)
JOURNAL	Langreil, S.R.H.
FEATURES	Unpublished
	Location/Qualifiers

source 1..466
/organism="Neonectria galligena"
/isolate="CBS 100318"
/db_xref="taxon:56674"
rRNA
gene 1..4
/gene="18S rRNA gene"
misc_RNA
gene 1..4
/gene="18S rRNA gene"
rRNA
gene 140..297
/note="internal transcribed spacer 1 (ITS 1)"
/gene="5.8S rRNA gene"
misc_RNA
gene 140..297
/note="internal transcribed spacer 2 (ITS 2)"
/gene="5.8S rRNA gene"
gene 463..466
/gene="28S rRNA gene"
BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtacggtctgcgt 18
||||| |||||||

Db 365 TCTAGTGGCGGTCTGCCT 382

RESULT 8
LOCUS NGA228663 466 bp RNA linear PLN 01-FEB-1999
DEFINITION Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA gene, and internal transcribed spacer 2 (ITS 2) (isolate CBS 100317).
ACCESSION AJ228663
VERSION AJ228663.1 GI:4210758
KEYWORDS 18S ribosomal RNA; 5.8S rRNA gene; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer; ITS1; ITS2.
SOURCE Neonectria galligena.
ORGANISM Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neonectria.
REFERENCE 1 (bases 1 to 466)
AUTHORS Langrell,S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-Apr-1998) Langrell, S.R.H., Department of Biological Sciences, Wye College, University of London, Wye, Ashford, Kent., TN25 5AH, UNITED KINGDOM
REFERENCE 2 (bases 1 to 466)
AUTHORS Langrell,S.R.H.
JOURNAL Unpublished
FEATURES
source location/Qualifiers
1..466
/organism="Neonectria galligena"
/isolate="CBS 100317"
/db_xref="taxon:56674"
rRNA
gene 1..4
/gene="18S rRNA gene"
misc_RNA
gene 1..4
/gene="18S rRNA gene"
rRNA
gene 140..297
/note="internal transcribed spacer 1 (ITS 1)"
/gene="5.8S rRNA gene"
misc_RNA
gene 140..297
/note="internal transcribed spacer 2 (ITS 2)"
/gene="5.8S rRNA gene"
gene 463..466
/gene="28S rRNA gene"
misc_RNA
gene 298..462

rRNA
gene 463..466
/gene="28S rRNA gene"
BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtacggtctgcgt 18
||||| |||||||

Db 365 TCTAGTGGCGGTCTGCCT 382

RESULT 9
LOCUS NGA228664 466 bp RNA linear PLN 01-FEB-1999
DEFINITION Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA gene, and internal transcribed spacer 2 (ITS 2) (isolate MUCL 40716).
ACCESSION AJ228664
VERSION AJ228664.1 GI:4210759
KEYWORDS 18S ribosomal RNA; 5.8S rRNA gene; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer; ITS1; ITS2.
SOURCE Neonectria galligena.
ORGANISM Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neonectria.
REFERENCE 1 (bases 1 to 466)
AUTHORS Langrell,S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-Apr-1998) Langrell, S.R.H., Department of Biological Sciences, Wye College, University of London, Wye, Ashford, Kent., TN25 5AH, UNITED KINGDOM
REFERENCE 2 (bases 1 to 466)
AUTHORS Langrell,S.R.H.
JOURNAL Unpublished
FEATURES
source location/Qualifiers
1..466
/organism="Neonectria galligena"
/isolate="MUCL 40716"
/db_xref="taxon:56674"
rRNA
gene 1..4
/gene="18S rRNA gene"
misc_RNA
gene 1..4
/gene="18S rRNA gene"
rRNA
gene 140..297
/note="internal transcribed spacer 1 (ITS 1)"
/gene="5.8S rRNA gene"
misc_RNA
gene 140..297
/note="internal transcribed spacer 2 (ITS 2)"
/gene="5.8S rRNA gene"
gene 298..462
/note="internal transcribed spacer 2 (ITS 2)"
/gene="28S rRNA gene"
BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tctagtacggtctgcgt 18
||||| |||||||

Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 10
NGA228665
LOCUS
DEFINITION NGA228665 466 bp RNA linear PLN 01-FEB-1999
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate MUCL
40782).

ACCESSION
VERSION AJ228665.1 GI:4210760
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.

SOURCE
ORGANISM Neonectria galligena.
Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
1 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
1.466
/organism="Neonectria galligena"
/isolate="MUCL 40782"
/db_xref="taxon:56674"
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1..4
/gene="18S rRNA gene"
5..139
/gene="18S rRNA gene"
misc_RNA /note="internal transcribed spacer 1 (ITS 1)"
140..297
/gene="5.8S rRNA gene"
140..297
/gene="5.8S rRNA gene"
298..462
/note="internal transcribed spacer 2 (ITS 2)"
463..>466
/gene="28S rRNA gene"
463..466
/gene="28S rRNA gene"
gene /gene="28S rRNA gene"
BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtgaaggtctgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 11
NGA228665
LOCUS
DEFINITION NGA228665 466 bp RNA linear PLN 01-FEB-1999
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate IMI
378754).

ACCESSION
VERSION AJ228666.1 GI:4210761
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.
Neonectria galligena.

ORGANISM Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.

REFERENCE
AUTHORS Langrell, S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
1.466
/organism="Neonectria galligena"
/isolate="IMI 378754"
/db_xref="taxon:56674"
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/gene="18S rRNA gene"
1..4
/gene="18S rRNA gene"
5..139
/gene="18S rRNA gene"
misc_RNA /note="internal transcribed spacer 1 (ITS 1)"
140..297
/gene="5.8S rRNA gene"
140..297
/gene="5.8S rRNA gene"
298..462
/note="internal transcribed spacer 2 (ITS 2)"
463..>466
/gene="28S rRNA gene"
463..466
/gene="28S rRNA gene"
BASE COUNT 107 a 142 c 111 g 106 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtgaaggtctgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 12
NGA228667
LOCUS
DEFINITION NGA228667 466 bp RNA linear PLN 01-FEB-1999
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate MUCL
40717).

ACCESSION
VERSION AJ228667.1 GI:4210762
KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.
Neonectria galligena.
Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
1 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)

REFERENCE
AUTHORS Langrell, S.R.H.
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
1.466
/organism="Neonectria galligena"

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/Isolate="MUCL 40717"
/db_xref="taxon:56674"
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rRNA
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1..4
gene
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5..139
misc_RNA
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rRNA
140..297
/gene="5.8S rRNA gene"
140..297
gene
/gene="5.8S rRNA gene"
238..462
misc_RNA
/Note="Internal transcribed spacer 2 (ITS 2)"
rRNA
463..>466
/gene="28S rRNA gene"
463..466
gene
/gene="28S rRNA gene"
107 a 142 c 111 g 106 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 8; Length 466;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 13
NGA228668
LOCUS
DEFINITION
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (Isolate MUCL
40784).
ACCESSION
AJ228668
VERSION
AJ228668.1 GI:4210763
KEYWORDS
18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.
SOURCE
Neonectria galligena.
Neonectria galligena.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE
Langrell,S.R.H.
AUTHORS
Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
JOURNAL
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)
REFERENCE
Langrell,S.R.H.
AUTHORS
Unpublished
JOURNAL
FEATURES
Location/Qualifiers
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/organism="Neonectria galligena"
/Isolate="MUCL 40784"
/db_xref="taxon:56674"
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/gene="18S rRNA gene"
1..4
gene
/gene="18S rRNA gene"
5..139
misc_RNA
/Note="Internal transcribed spacer 1 (ITS 1)"
rRNA
140..297
/gene="5.8S rRNA gene"
140..297
gene
/gene="5.8S rRNA gene"
238..462
misc_RNA
/Note="Internal transcribed spacer 2 (ITS 2)"
rRNA
463..>466

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/gene="28S rRNA gene"
463..466
gene
/gene="28S rRNA gene"
107 a 142 c 111 g 106 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 8; Length 466;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

RESULT 14
NGA228669
LOCUS
DEFINITION
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (Isolate ICMP
13269).
ACCESSION
AJ228669
VERSION
AJ228669.1 GI:4210764
KEYWORDS
18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
ITS1; ITS2.
SOURCE
Neonectria galligena.
Neonectria galligena.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE
Langrell,S.R.H.
AUTHORS
Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
JOURNAL
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
2 (bases 1 to 466)
REFERENCE
Langrell,S.R.H.
AUTHORS
Unpublished
JOURNAL
FEATURES
Location/Qualifiers
1..466
/organism="Neonectria galligena"
/Isolate="ICMP 13269"
/db_xref="taxon:56674"
<1..4
rRNA
/gene="18S rRNA gene"
1..4
gene
/gene="18S rRNA gene"
5..139
misc_RNA
/Note="Internal transcribed spacer 1 (ITS 1)"
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/gene="5.8S rRNA gene"
140..297
gene
/gene="5.8S rRNA gene"
238..462
misc_RNA
/Note="Internal transcribed spacer 2 (ITS 2)"
rRNA
463..>466
/gene="28S rRNA gene"
463..466
gene
/gene="28S rRNA gene"
107 a 142 c 111 g 106 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 94.4%; Score 16.4; DB 8; Length 466;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tctagtacggtctcgct 18
||||| |||||||
Db 365 TCTAGTGGCGTCTCGCT 382

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```

RESULT 15
LOCUS   NGA228670               466 bp    RNA      linear    PLN 01-FEB-1999
DEFINITION
Nectria galligena internal transcribed spacer 1 (ITS 1), 5.8S rRNA
gene, and internal transcribed spacer 2 (ITS 2) (isolate CBS
100325).
ACCESSION
AJ228670.1   GI:4210765
VERSION
18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;
5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer;
ITS1; ITS2.
SOURCE
Neonectria galligena.
ORGANISM
Neonectria galligena
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Neonectria.
REFERENCE
1 (bases 1 to 466)
Langrell,S.R.H.
AUTHORS
Direct Submission
TITLE
Submitted (07-APR-1998) Langrell, S.R.H., Department of Biological
Sciences, Wye College, University of London, Wye, Ashford, Kent.,
TN25 5AH, UNITED KINGDOM
JOURNAL
2 (bases 1 to 466)
Langrell,S.R.H.
REFERENCE
Unpublished
FEATURES
Location/Qualifiers
     source             1..466
                        /organism="Neonectria galligena"
                        /isolate="CBS 100325"
                        /db_xref="taxon:56674"
                        <1..4
                        /gene="18S rRNA gene"
                        1..4
                        /gene="18S rRNA gene"
                        5..139
                        /note="Internal transcribed spacer 1 (ITS 1)"
                        140..297
                        /gene="5.8S rRNA gene"
                        140..297
                        /gene="5.8S rRNA gene"
                        298..462
                        /note="Internal transcribed spacer 2 (ITS 2)"
                        463..>466
                        /gene="28S rRNA gene"
                        463..466
                        /gene="28S rRNA gene"
BASE COUNT   107 a      142 c      111 g      106 t
ORIGIN

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Query Match          91.18; Score 16.4; DB 8; Length 466;
Best Local Similarity 94.48; Pred. NO. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Caps 0;
QY 1 tctagtgcaggtctcgct 18
   ||||| ||||| |||||
Db 365 TCTAGTGCAGGCTCTCGCT 382

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 Job time: 14204 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:42 ; Search time 594.49 Seconds
(without alignments)
51.985 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 18

Sequence: 1 tctagtgacggtctcgt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	20	AAV83696
2	16.4	91.1	310	20	AAV70851
3	16.4	91.1	502	21	AA61893
4	16.4	91.1	2293	23	AA516211
5	15.4	85.6	744	21	AA642796
6	15	83.3	1182	19	AA799142
7	15	83.3	1596	23	AA588320
8	14.8	82.2	506	22	AA080445
9	14.8	82.2	1502	22	AA080412
					Human secreted pro

10	14.4	80.0	51	22	AA174530
11	14.4	80.0	51	22	AA174531
12	14.4	80.0	945	22	AAH3958
13	14.4	80.0	1146	22	AAH53831
14	14.4	80.0	2982	22	AAH54021
15	14.4	80.0	3116	22	AAH54884
16	14.4	80.0	46899	15	AA054386
17	14	77.8	479	22	ABA75543
18	14	77.8	479	22	ABA40157
19	14	77.8	479	22	AAK24114
20	14	77.8	479	22	AAK50175
21	14	77.8	479	22	AA127255
22	14	77.8	479	22	AA156113
23	14	77.8	489	22	ABA08494
24	14	77.8	550	22	ABA65091
25	14	77.8	550	22	ABA30343
26	14	77.8	550	22	AAK11513
27	14	77.8	550	22	AAK37292
28	14	77.8	550	22	AA181119
29	14	77.8	550	22	AA143123
30	14	77.8	615	15	AA062632
31	14	77.8	636	17	AA787815
32	14	77.8	639	16	AA080291
33	14	77.8	642	20	AA228805
34	14	77.8	645	16	AA080293
35	14	77.8	649	21	AA259451
36	14	77.8	666	15	AA073443
37	14	77.8	666	17	AA787817
38	14	77.8	699	22	AAH77315
39	14	77.8	717	16	AA092504
40	14	77.8	735	16	AA092500
41	14	77.8	735	16	AA092502
42	14	77.8	777	17	AA742507
43	14	77.8	780	21	AA427848
44	14	77.8	798	13	AA030706
45	14	77.8	798	15	AA044642

ALIGNMENTS

RESULT	1
AAV83696	
ID	AAV83696 standard; DNA; 18 BP.
XX	
AC	AAV83696;
XX	
DT	26-FEB-1999 (first entry)
XX	
DE	Species-specific probe targeted to the internal transcribed spacer 2.
XX	
KM	Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus;
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KM	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW	M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KM	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KM	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Synthetic.
OS	Fusarium moniliforme.
XX	
FH	Key
FT	modified_base 1
FT	Location/Qualifiers
FT	/*tag- 2
FT	/note- "labelled with digoxigenin"
PN	W09850584-A2.
XX	
PD	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US08926.
XX	

Human silent SNP c
Human silent SNP c
S. epidermidis ope
S. epidermidis ope
S. epidermidis gen
S. epidermidis gen
T. nelsoni Cyclospo
Human foetal liver
Probe #18623 for g
Human brain expres
Human bone marrow
Probe #17188 for g
Probe #24799 used
Human Fc-gamma rec
Human foetal liver
Probe #8809 for ge
Human brain expres
Human bone marrow
Probe #8052 for ge
Probe #11809 used
Porphyria antibody
Antibody 7612 heav
Monoclonal antibod
Coding sequence fo
Monoclonal antibod
Antibody Fab fragm
6D9 antibody heavy
Antibody 3G2 heavy
19G Fab-BPI fusion
Mouse antibody H3-
Mouse antibody FB3
Murine antibody F4-
Murine A5B57 Fd fr
HOM-1 Fab heavy ch
Sequence of clone
Fd phage clone seq

```

PR 02-MAY-1997; 97US-0045400.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX WPI: 1999-034737/03.
XX
XX New nucleic acid probes for filamentous fungi - for detecting e.g.
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
XX species.
XX
XX Example 1: Page 22; 45pp; English.
XX
XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
XX (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
XX are species-specific, and can be used for identifying a species selected
XX from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A.
XX nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M.
XX plumbeus, M. indicus, M. circinelloides f. circinelloides, Rhizopus
XX oryzae, R. microsporus, R. circinans, R. stolonifer, Rhizomucor
XX pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallescheria
XX boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
XX Sporothrix schenckii. The probes can be used for differentiating
XX filamentous fungal species from each other and from other medically
XX important fungi.
XX
XX Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 18; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 tctagtgcgcgtcgcgt 18
XX ||||||| |||||||
XX Db 1 tctagtgcgcgtcgcgt 18
XX
XX
XX RESULT 2
XX ID AAV70851
XX AAV70851 standard; DNA; 310 BP.
XX
XX AAV70851;
XX 26-FEB-1999 (first entry)
XX
XX Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX
XX Internal transcribed spacer 2; ITS2; probe; Aspergillus flavus;
XX A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
XX Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
XX M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
XX R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
XX Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
XX Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX
XX Fusarium moniliforme.
XX
XX WO9850584-A2.
XX
XX 12-NOV-1998.
XX
XX 01-MAY-1998; 98WO-US08926.
XX
XX 02-MAY-1997; 97US-0045400.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX WPI: 1999-034737/03.
XX

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XX
XX New nucleic acid probes for filamentous fungi - for detecting e.g.
XX Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
XX Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
XX species.
XX
XX Claim 1; Page 12; 45pp; English.
XX
XX The present sequence represents an internal transcribed spacer 2 (ITS2)
XX and adjacent regions. Probes can be derived from the present sequence
XX which are species-specific. The specification also describes ITS2
XX sequence-derived probes for identifying a species selected from
XX Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
XX Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
XX M. indicus, M. circinelloides f. circinelloides, Rhizopus oryzae,
XX R. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus,
XX Absidia corymbifera, Cunninghamella elegans, Pseudallescheria boydii
XX (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
XX Sporothrix schenckii. The probes can be used for differentiating
XX filamentous fungal species from each other and from other medically
XX important fungi.
XX
XX Sequence 310 BP; 73 A; 86 C; 80 G; 71 T; 0 other;
XX
XX
XX Query Match 91.1%; Score 16.4; DB 20; Length 310;
XX Best Local Similarity 94.4%; Pred. No. 19;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 1 tctagtgcgcgtcgcgt 18
XX ||||||| |||||||
XX Db 174 tctagtgcgcgtcgcgt 191
XX
XX
XX RESULT 3
XX ID AAA61893
XX AAA61893 standard; DNA; 502 BP.
XX
XX AAA61893;
XX
XX 14-NOV-2000 (first entry)
XX
XX Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX
XX Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
XX HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
XX acquired immunodeficiency syndrome; AIDS; AIDS-related complex;
XX symptomatic infection; asymptomatic infection; potential HIV exposure;
XX combination therapy; ds.
XX
XX Fusarium sp. MF6381.
XX
XX WO200036132-A1.
XX
XX 22-JUN-2000.
XX
XX 09-DEC-1999; 99WO-US29356.
XX
XX 14-DEC-1998; 98US-0112168.
XX
XX (MERT ) MERCK & CO INC.
XX
XX Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
XX Dombrowski AW;
XX WPI: 2000-431606/37.
XX
XX New steroid compounds are HIV integrase inhibitors used for treating
XX HIV infection and AIDS -
XX
XX Disclosure: Page 14; 113pp; English.
XX
XX The invention relates to novel steroid compounds derived from the
XX

```

CC African soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as
CC inhibitors of HIV integrase. The invention encompasses cultures of
CC *Fusarium* sp. MF6381. The invention also relates to a composition
CC comprising a compound of the invention in combination with an AIDS
CC antiviral agent, an immunomodulator and an antineoplastic agent. The
CC compounds of the invention may be used in the inhibition of HIV
CC integrase and in the prevention and treatment of HIV infection. A wide
CC range of state of HIV infection may be treated: AIDS (acquired
CC immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic
CC and asymptomatic HIV infection; and actual or potential exposure to HIV.
CC The compounds may be used to isolate HIV integrase mutants which are
CC potentially useful as screening tools for antiviral compounds. The
CC compounds may also be used to establish or determine the site at which
CC other antivirals bind to HIV integrase (e.g., by competitive inhibition).
CC The present sequence represents the ribosomal DNA (rDNA) internal
CC transcribed spacer (ITS) region of *Fusarium* sp. MF6381, which may be used
CC to characterize MF6381.
XX
SO Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 other;

Query Match 91.1%; Score 16.4; DB 21; Length 502;
Best Local Similarity 94.4%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtgcggtctcgct 18
||||||| |||||||||
Db 371 tctagtgcggtctcgct 388

RESULT 4
AAS16211
ID AAS16211 standard; DNA: 2293 BP.
XX AAS16211:
XX
DT 29-JAN-2002 (first entry)
XX
DE Fungus genomic DNA spanning 18S, 5.8S and 28S rRNA and ITS sequences.
XX
KW Gibberellin; 18S rRNA; internal transcribed spacer region; ITS1;
KW ITS2; 5.8S rRNA; LTR-1027; species differentiation; GA_4; GA_3; GA_7;
KW flowering; fruit cell elongation; apple; pear; grape; fruit;
KW russet control; fungus; ds.
XX
OS *Gibberella fujikuroi*.
XX
FH Key Location/Qualifiers
FT misc_feature 1..1774
FT /*tag= a
FT /note= "18S rRNA gene"
FT 1775..1921
FT /*tag= b
FT /note= "ITS1 region"
FT 1922..2078
FT /*tag= c
FT /note= "5.8S rRNA gene"
FT 2079..2243
FT /*tag= d
FT /note= "ITS2 region"
FT 2244..2293
FT /*tag= e
FT /note= "28S rRNA gene"
XX
PN US6287800-B1.
XX
PD 11-SEP-2001.
XX
PP 23-AUG-2000; 2000US-0645073.
XX
PR 31-AUG-1999; 99US-151770P.
XX
PA (GALL/) GALLAZZO J L.

PA (LEEM/) LEE M D.
XX
PI Gallazzo JL, Lee MD;
XX
DR WPI: 2001-662197/76.
XX
PT A new method for producing a mixture of gibberellins from *Gibberella*
PT *fujikuroi* results in high titers of GA4 and GA7 useful to promote
PT flowering and fruit growth in the fruit growing industry.
XX
PS Example 4: Column 9-12; 7pp; English.
XX
CC This sequence represents a genomic DNA sequence containing the 18S rRNA
CC gene, internal transcribed spacer regions 1 and 2 (ITS1, ITS2) and 5.8S
CC rRNA sequences from a mutant strain of *Gibberella fujikuroi* (LTR-1027)
CC of the invention. This region of DNA is highly variable and can be used
CC for species and strain differentiation. The LTR-1027 mutant produces a
CC mixture of gibberellins which is at least 70 % GA_4 and GA_7.
CC *Gibberellins* GA_4 and GA_7 promote flowering and fruit cell elongation,
CC and are used by growers of apples, pears and grapes to produce larger
CC fruits and earlier harvests. The mixture of GA_3, GA_4 and GA_7 achieved
CC using the method of this invention should be particularly useful in the
CC apple industry where GA_4 has been found more effective in russet
CC control and in promoting fruit set. This method produces GA_4 and GA_7
CC in much higher titers than prior art methods.
XX
SO Sequence 2293 BP; 596 A; 527 C; 592 G; 578 T; 0 other;

Query Match 91.1%; Score 16.4; DB 23; Length 2293;
Best Local Similarity 94.4%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtgcggtctcgct 18
||||||| |||||||||
Db 2145 tctagtgcggtctcgct 2162

RESULT 5
AAC42796
ID AAC42796 standard; DNA: 744 BP.
XX
AC AAC42796;
XX
DT 17-OCT-2000 (first entry)
XX
DE *Arabidopsis thaliana* DNA fragment SEQ ID NO: 36883.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS *Arabidopsis thaliana*.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PP 25-FEB-2000; 2000EP-0301439.
XX
PR 05-MAR-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128645.
PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130510.

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PR 30-APR-1999; 99US-0132407.
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PR 06-MAY-1999; 99US-0132486.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 22-JUN-1999; 99US-0139899.
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PR 08-JUL-1999; 99US-0142803.
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PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.

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PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151066.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161922.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

```

Query Match 85.6%; Score 15.4; DB 21; Length 744;
 Best Local Similarity 94.1%; Pred. No. 70;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 2 ctatgacgctcgcct 18
   ||||| ||||| ||||| |||||
DB 218 ctatgacgctcgcct 234

```

RESULT 6
 AAT99142/C
 ID AAT99142 standard; cDNA to mRNA; 1182 BP.

```

XX AC AAT99142;
XX DT 26-MAR-1998 (first entry)
XX DE S-adenosylmethionine synthase 2 gene.
XX KW S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
XX sam2; ss.
XX OS Hordeum vulgare.
XX PN JP09313186-A.
XX PD 09-DEC-1997.
XX PF 28-MAY-1996: 96JP-0133406.
XX PR 28-MAY-1996: 96JP-0133406.
XX PA (NIOC ) NIPPON OIL CO LTD.
XX DR WPI: 1998-080077/08.
XX DR P-PSDB; AAM34541.
XX PT S-adenosyl-methionine synthase gene - useful in producing plants
XX PT resistant to alkaline soil
XX PS Claim 5; Page 9-10; 13pp; Japanese.
XX CC This sequence represents the S-adenosylmethionine synthase 2 (sam2)
XX CC gene. This DNA sequence may be used in a vector to produce plants which
XX CC are resistant to alkaline soil.
SQ Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

```

Query Match 83.3%; Score 15; DB 19; Length 1182;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 taatgacgctcgc 17
   ||||| ||||| |||||
DB 145 TAGTACGCTCGC 131

```

RESULT 7
 AAS88320
 ID AAS88320 standard; cDNA; 1596 BP.

```

XX AC AAS88320;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #24124.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB; ABG24133.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1; SEQ ID NO 24124; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations in
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 1596 BP; 405 A; 350 C; 462 G; 379 T; 0 other;

```

Query Match 83.3%; Score 15; DB 23; Length 1596;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
Oy      4 agtgcggtctgcgt 18
          |||||
Db      1378 agtgcggtctgcgt 1392

RESULT 8
AAD08445/c
ID      AAD08445 standard; cDNA; 506 BP.
XX
AC      AAD08445;
XX
DT      09-AUG-2001 (first entry)
XX
DE      Human secreted protein-encoding gene 9 cDNA clone HOVAF78, SEQ ID NO:52.
XX
KW      Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW      foetal abnormality; developmental abnormality; haematopoietic disorder;
KW      immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW      Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW      portalis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW      inflammation; neurological disorder; Alzheimer's disease; food additive;
KW      angiotensin-related disorder; kidney disorder; gastrointestinal disorder; allergy;
KW      pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW      cell culture; chemotaxis; vulnerability; binding partner identification;
KW      gene therapy; chromosome 19; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FH      CDS
FT      269..505
FT      /*tag- a
FT      /product- "Human secreted protein precursor"
FT      /transl_except- (pos:311..313, aa:Xaa)
FT      /transl_except- (pos:329..331, aa:Xaa)
FT      /transl_except- (pos:413..415, aa:Xaa)
FT      /transl_except- (pos:461..463, aa:Xaa)
FT      /transl_except- (pos:464..466, aa:Xaa)
FT      /note- "Xaa equals any of the naturally occurring
FT      L-amino acids; CDS does not include stop codon"
FT      /partial
FT      sig_peptide
FT      269..322
FT      /*tag- b
FT      mat_peptide
FT      323..505
FT      /*tag- c
FT      /product- "Mature human secreted protein"
XX
PN      WO200134643-A1.
XX
PD      17-MAY-2001.
XX
PF      08-NOV-2000; 2000MO-US30629.
XX
PR      12-NOV-1999; 99US-0164825.
PR      03-AUG-2000; 2000US-0222904.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
XX
DR      P-PSDB; AAEO4140.
XX
PT      Nucleic acids encoding 24 human secreted polypeptides, useful for
PT      preventing, diagnosing and/or treating e.g. Gaucher's disease,
PT      Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease,
PT      diabetes mellitus and multiple sclerosis -
XX
PS      Claim 1; Page 445; 532pp; English.
XX
CC      AAD08404-AAD08478 represent cDNAs corresponding to 24 human secreted
CC      protein genes, and AAEO4100-AAEO4170 represent the proteins they encode.
CC      AAEO4172-AAEO4197 represent human secreted protein fragments or variants.
```

```
CC      The secreted proteins and their genes are useful for preventing, treating
CC      or ameliorating medical conditions, e.g., by protein or gene therapy.
CC      Pathological conditions can be diagnosed by determining the amount of the
CC      new protein in a sample or by determining the presence of mutations in
CC      the new genes. Specific uses are described for each of the 24 genes,
CC      based on the tissues in which they are most highly expressed, and include
CC      developing products for the diagnosis or treatment of proliferative
CC      disorders, cancer, tumours, foetal and developmental abnormalities,
CC      haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
CC      diseases (e.g., rheumatoid arthritis), inflammation, allergies,
CC      neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
CC      cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
CC      psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
CC      angiotensin-related disorders, kidney disorders, gastrointestinal disorders,
CC      pregnancy-related disorders, endocrine disorders, and infections. The
CC      proteins can also be used to aid wound healing and epithelial cell
CC      proliferation, to prevent skin aging due to sunburn, to maintain organs
CC      before transplantation, for supporting cell culture of primary tissues,
CC      to regenerate tissues, to identify their cognate ligands or binding
CC      partners, and in chemotaxis, and can be used as a food additive or
CC      preservative to modify storage properties. Antibodies specific for a
CC      protein of the invention can be used in alleviating symptoms associated
CC      with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC      radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC      The present sequence represents a human secreted protein-encoding cDNA of
CC      the invention.
XX
SQ      Sequence 506 BP; 134 A; 117 C; 122 G; 128 T; 5 other;

Query Match      82.2%; Score 14.8; DB 22; Length 506;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 tctagtcggtctgcgt 18
          ||| ||| ||| ||| ||| |||
Db      379 TCTGTTGAAGCTCTCGCT 362

RESULT 9
AAD08412/c
ID      AAD08412 standard; cDNA; 1502 BP.
XX
AC      AAD08412;
XX
DT      09-AUG-2001 (first entry)
XX
DE      Human secreted protein-encoding gene 9 cDNA clone HOVAF78, SEQ ID NO:19.
XX
KW      Human; secreted protein; proliferative disorder; cancer; tumour; asthma;
KW      foetal abnormality; developmental abnormality; haematopoietic disorder;
KW      immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW      Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;
KW      portalis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;
KW      inflammation; neurological disorder; Alzheimer's disease; food additive;
KW      angiotensin-related disorder; kidney disorder; gastrointestinal disorder; allergy;
KW      pregnancy-related disorder; endocrine disorder; infection; wound healing;
KW      cell culture; chemotaxis; vulnerability; binding partner identification;
KW      gene therapy; chromosome 19; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FH      CDS
FT      269..481
FT      /*tag- a
FT      /product- "Human secreted protein precursor"
FT      /transl_except- (pos:311..313, aa:Xaa)
FT      /transl_except- (pos:329..331, aa:Xaa)
FT      /transl_except- (pos:413..415, aa:Xaa)
FT      /transl_except- (pos:461..463, aa:Xaa)
FT      /transl_except- (pos:464..466, aa:Xaa)
FT      /note- "Xaa equals any of the naturally occurring
FT      L-amino acids; CDS does not include stop codon"
FT      /partial
FT      sig_peptide
FT      269..322
FT      /*tag- b
FT      mat_peptide
FT      323..478
FT      /*tag- c
FT      /product- "Mature human secreted protein"
XX
PN      WO200134643-A1.
```

PX	17-MAY-2001.
PD	
XX	08-NOV-2000; 2000OWO-US30629.
XX	
PR	12-NOV-1999; 99US-0164825.
PR	03-AUG-2000; 2000US-0222904.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
P1	Ruben SM, Komatsoulis GA, Soppet DR, Shi Y;
PT	WPI: 2001-374441/39.
DR	P-PSDB: AAE04108.
XX	
PT	Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis -
PS	Claim 1; Page 421-422; 532pp; English.
XX	
CC	AAD08404-AA008478 represent cDNAs corresponding to 24 human secreted protein genes, and AAE04100-AAE004170 represent the proteins they encode.
CC	AAE04112-AAE04197 represent human secreted protein fragments or variants.
CC	The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.
CC	Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiotensin-related disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The protein can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or a preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
CC	The present sequence represents a human secreted protein-encoding cDNA of the invention.
CC	
SO	Sequence 1502 BP; 377 A; 340 C; 338 G; 447 T; 0 other;
XX	
Query Match	82.2%; Score 14.8; DB 22; Length 1502;
Best Local Similarity	88.9%; Pred. No.1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0.	
OY	1 tctagtgcggtcgcgt 18
Db	379 TCTGGTGAAGGCTCGCT 362
RESULT 10	
AAI74530	
ID	AAI74530 standard; DNA: 51 BP.
XX	
AC	AAI74530;
XX	
DT	09-NOV-2001 (first entry)
XX	
DE	Human silent SNP containing nucleic acid SEQ:1471.

[illegible]

OS Homo sapiens.
XX WO200140521-A2.
PN 07-JUN-2001.
XX 30-NOV-2000; 2000WO-US32758.
PF 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX (CURA-) CURAGEN CORP.
XX Shinkets RA, Leach M;
PI WPI: 2001-356160/37.
DR Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy -
PT Claim 1: Page 504; 2653pp; English.
PS
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acid
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 22 A; 11 C; 11 G; 7 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 51;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtgcgctcgc 16
DB 29 tctagtgcgctcgc 44

RESULT 12
ID AAH53958/c
XX AAH53958 standard; DNA; 945 BP.
AC AAH53958:
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3309.
XX
KM Staphylococcus epidermidis SRI strain; Infection; diagnosis;
XX vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX

PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Kimmery MJ;
XX
DR WPI: 2001-316495/33.
DR P-FSDB; AAG83108.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
PS Claim 8; Page 872; 2188pp; English.
XX
XX AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
XX no sequences are present for SEQ ID NO:4455 to 4464.
SQ Sequence 945 BP; 356 A; 139 C; 201 G; 249 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 945;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctagtgcgctcgc 17
DB 268 ctactgcgctcgc 253

RESULT 13
ID AAH53831/c
XX AAH53831 standard; DNA; 1146 BP.
AC AAH53831:
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3055.
XX
KM Staphylococcus epidermidis SRI strain; Infection; diagnosis;
XX vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.

XX kimmerly wj;
PI WPI: 2001-316495/33.
DR P-PDB: AAG82981.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PS useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 8: Page 804: 2188pp: English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 1146 BP; 437 A; 168 C; 230 G; 311 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 1146;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctactgacggtctcgc 17
||| |||||
Db 469 CTACTGACGCTCTCGC 454

RESULT 14
AAH54021
ID AAH54021 standard; DNA: 2982 BP.
XX
AC AAH54021;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3385.
XX
KW Staphylococcus epidermidis SRI strain; Infection; diagnosis;
KM vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI kimmerly wj;
XX
PS WPI: 2001-316495/33.
XX

PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 8: Page 938-939; 2188pp: English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 2982 BP; 753 A; 592 C; 434 G; 1203 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 2982;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctactgacggtctcgc 17
||| |||||
Db 1311 ctactgacggtctcgc 1326

RESULT 15
AAH54884
ID AAH54884 standard; DNA: 3116 BP.
XX
AC AAH54884;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4248.
XX
KW Staphylococcus epidermidis SRI strain; Infection; diagnosis;
KM vaccination; endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI kimmerly wj;
XX
PS WPI: 2001-316495/33.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
PT useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 8: Page 1970-1971; 2188pp: English.
XX
CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides

CC (11), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
 CC (1) and (11) can have antibacterial activity and therefore can be used
 CC in vaccination. The nucleic acids (I) may be used to produce the
 CC *S. epidermidis* polypeptides (II) via the production of vectors
 CC containing them which are used to produce hosts cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to
 CC AAH5090 represent specifically claimed *S. epidermidis* genomic DNA
 CC polynucleotide sequences from the present invention. AAH5091 to
 CC AAH5098 represent oligonucleotide sequences and primers which are used
 CC in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the polynucleotide
 CC sequences given in the sequence listing of the present specification,
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
 CC no sequences are present for SEQ ID NO:4455 to 4464.
 CC
 XX
 SO Sequence 3116 BP; 966 A; 578 C; 454 G; 1118 T; 0 other;

Query Match 80.08; Score 14.4; DB 22; Length 3116;
 Best Local Similarly 93.8%; Pred. No. 2.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 ctatgacggtctcgc 17
 ||| |||||
 Db 1615 ctactgacggtctcgc 1630

Search completed: August 21, 2002, 22:22:44
 Job time: 5784 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32.13 ; Search time 5019.06 Seconds
(without alignments)
48.405 Million cell updates/sec

Title: US-10-046-955-49

Sequence: 1 tctagtgcgcgtcgcgc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estdb:*
2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_hlc:*
13: em_gss_hum:*
14: em_gss_liv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	936	12	CNS03M43 AL250284 Tetraodon
2	15.4	85.6	481	12	BH625357 BH625357 100710660
3	15.4	85.6	486	10	BE784335 BE784335 601473468
4	15.4	85.6	628	10	BUI30132 BUI30132 601473468
5	15.4	85.6	629	10	BUI47480 BUI47480 60147480
6	15.4	85.6	703	9	AU004847 AU004847 60147480
7	15.4	85.6	718	9	AV398645 AV398645 6022717012
8	15.4	85.6	1005	10	BG760845 BG760845 6022717012
9	15.4	85.6	1311	10	BG757034 BG757034 6022710452
10	15.4	83.3	112	9	AV940706 AV940706 6022710452
11	15.4	83.3	168	9	AV922948 AV922948 6022710452
12	15.4	83.3	241	9	AA324668 AA324668 6022710452
13	15.4	83.3	256	9	AA367189 AA367189 6022710452
14	15.4	83.3	276	9	AA339193 AA339193 6022710452
15	15.4	83.3	329	9	AM351943 AM351943 6022710452
16	15.4	83.3	360	12	TA301E06P AL490856 T. Brucei
17	15.4	83.3	362	10	N49663 yv26d12.rl

18	83.3	369	10	BF438464 BF438464 7p82h06.x
19	83.3	370	9	AA324673 AA324673 EST27824
20	83.3	375	9	AL134474 AL134474 DKP2P547K
21	83.3	398	10	H20232 H20232 yns6d08.rl
22	83.3	400	10	BG119356 BG119356 602349035
23	83.3	406	9	AI347337 AI347337 LC05903.x
24	83.3	411	9	AV939224 AV939224 AV939224
25	83.3	427	10	BI461101 BI461101 603206979
26	83.3	430	10	BE438640 BE438640 BCD102.WH
27	83.3	442	10	BE868742 BE868742 601445978
28	83.3	445	10	BM377636 BM377636 EDEM04.SQ
29	83.3	447	10	BM369940 BM369940 EBY008.SQ
30	83.3	460	10	BI756944 BI756944 603029151
31	83.3	462	10	BF038758 BF038758 601461250
32	83.3	466	10	BE262001 BE262001 601153682
33	83.3	469	12	AO685141 AO685141 HS_2160.A
34	83.3	470	10	W05422 W05422 2a83e11.rl
35	83.3	478	10	BI334225 BI334225 602997728
36	83.3	484	10	BE513967 BE513967 601315813
37	83.3	488	10	BG700095 BG700095 602679454
38	83.3	490	10	BI836611 BI836611 603089596
39	83.3	493	10	BG424777 BG424777 602453425
40	83.3	493	10	BF630275 BF630275 HVSMBD00
41	83.3	495	10	BG707736 BG707736 602671257
42	83.3	503	10	BI771378 BI771378 603059392
43	83.3	503	10	BI818791 BI818791 603037641
44	83.3	505	9	AM672790 AM672790 ba01e11.y
45	83.3	506	9	AA182515 AA182515 zp54e04.r

ALIGNMENTS

RESULT 1
CNS03M43
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
037103 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
AL250284
VERSION
AL250284.1 GI:7971296
KEYWORDS
GSS: genome survey sequence.
SOURCE
Tetraodon nigroviridis.
ORGANISM
Tetraodon nigroviridis

REFERENCE
AUTHORS
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Weissenbach,U.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 936)

REFERENCE
AUTHORS
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Queller,F.,
Saurin,W. and Weissenbach,U.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 936)

REFERENCE
AUTHORS
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Queller,F.,
Saurin,W. and Weissenbach,U.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 936)

FEATURES
source
Location/Qualifiers
1..936
/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"
 /clone_11b="G"
 /note="Genoscope sequence ID : C0BG037AE02LP1-end : 77"
 BASE COUNT 174 a 259 c 267 g 236 t
 ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 936;
 Best Local Similarity 94.4%; Pred. No. 4.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cttagtgcagctcgcct 18
 |||
 Db 168 TCCAGTACGCGCTCGCT 185

RESULT 2
 BH625357/c 481 bp DNA linear GSS 30-JAN-2002
 LOCUS 1007106H02.y1 1007 - Rescuemu Grid H zea mays genomic, DNA
 DEFINITION sequence.
 ACCESSION BH625357 GI:18438608
 VERSION BH625357.1 GI:18438608
 KEYWORDS GSS.
 SOURCE zea mays.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 1 (bases 1 to 481)
 REFERENCE Walbot,V.
 TITLE Maize genomic sequences found using engineered Rescuemu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1007106 column: 29
 Class: transposon-tagged.
 Location/Qualifiers
 1..481
 /organism="Zea mays"
 /cultivar="mixed background W23/A18/B73"
 /db_xref="taxon:4577"
 /clone_11b="1007 - Rescuemu Grid H"
 /tissue-type="leaf"
 /dev-stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescuemu (engineered from Bluescript backbone); Site_1: BamHI; Site_2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 68 a 193 c 127 g 93 t
 ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 481;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 cttagtgcagctcgcct 18
 |||
 Db 410 CTAGTACGCGCTCGCT 394

RESULT 3
 BE784335/c 486 bp mRNA linear EST 20-OCT-2000
 LOCUS 601473488F1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3876716 5',
 DEFINITION mRNA sequence.
 ACCESSION BE784335
 VERSION BE784335.1 GI:10205533
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 486)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP/Gazdar
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LAM637 row: 0 column: 21
 High quality sequence stop: 160.
 Location/Qualifiers
 1..486
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3876716"
 /clone_11b="NIH_MGC_68"
 /tissue-type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: PCMV-SpORF6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 196 a 100 c 92 g 98 t
 ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 486;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 cttagtgcagctcgcct 18
 |||
 Db 232 CAACTGACGCGCTCGCT 216

RESULT 4
 BJI30132 626 bp mRNA linear EST 23-JAN-2002
 LOCUS BJI30132 unpublished oligo-capped CDNA library, C. elegans L1 stage
 DEFINITION Caenorhabditis elegans CDNA clone yk1039d08 3', mRNA sequence.
 ACCESSION BJI30132
 VERSION BJI30132.1 GI:18290289
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloiderinae; Caenorhabditis.
 1 (bases 1 to 626)
 REFERENCE Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.

TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 626
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1039d08"
/clone_1lb="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/dev_stage="L1"

BASE COUNT 151 a 145 c 135 g 190 t 5 others
ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 626;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgct 18
||| ||||| |||||
Db 455 TCNAGTGACGGCTCGCT 472

RESULT 5
LOCUS BJ147480 629 bp mRNA linear EST 24-JAN-2002
DEFINITION BJ147480 unpublished oligo-capped cDNA library, C. elegans L1 stage
ACCESSION BJ147480
VERSION BJ147480.1 GI:18315465
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Telodermidae; Caenorhabditis.
1 (bases 1 to 629)
Kohara, Y., Shin-1, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 629
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1251f07"
/clone_1lb="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/dev_stage="L1"

BASE COUNT 151 a 146 c 133 g 192 t 7 others
ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 629;

Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgct 18
||| ||||| |||||
Db 456 TCNAGTGACGGCTCGCT 473

RESULT 6
LOCUS AU004847/c 703 bp mRNA linear EST 19-JAN-1999
DEFINITION AU004847 Bombyx mori p50(Daizo) Bombyx mori cDNA clone ws20913,
mRNA sequence.
ACCESSION AU004847
VERSION AU004847.1 GI:4162218
KEYWORDS EST.
SOURCE domestic silkworm.
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 703)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Establishment of cDNA database of Bombyx mori
Unpublished (1999)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: km1ta@nirs.go.jp
PROJECT = 'CREST project by JST'.
Location/Qualifiers

FEATURES
source
1. 703
/organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws20913"
/clone_1lb="Bombyx mori p50(Daizo)"

BASE COUNT 182 a 142 c 145 g 234 t
ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 703;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgct 17
||| ||||| |||||
Db 491 TCTACTGACGGCTCTAGC 475

RESULT 7
LOCUS AV398645/c 718 bp mRNA linear EST 05-FEB-2000
DEFINITION AV398645 Bombyx mori ovary bmnPV infected: 6 hr after inoculation
Bombyx mori cDNA clone NV060125 T3, mRNA sequence.
ACCESSION AV398645
VERSION AV398645.1 GI:6902297
KEYWORDS EST.
SOURCE domestic silkworm.
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 718)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: km1ta@nirs.go.jp

ACCESSION	CDNA clone bah28115 5', mRNA sequence.
VERSION	AV940706
KEYWORDS	AV940706.1 GI:18236503
SOURCE	EST.
ORGANISM	Hordeum vulgare subsp. spontaneum.
REFERENCE	Hordeum vulgare subsp. spontaneum
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
JOURNAL	; Trilicaceae; Hordeum.
COMMENT	1 (bases 1 to 112) Sato, K., Saisho, D. and Takeda, K. Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002) Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp. Location/Qualifiers 1..112
FEATURES	/organism="Hordeum vulgare subsp. spontaneum" source /strain="H602" /db_xref="taxon:77009" /clone="bah28115" /clone_1lb="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage" 25 a 34 c 32 g 20 t 1 others
BASE COUNT	25 a 34 c 32 g 20 t 1 others
ORIGIN	
Query Match	83.3%; Score 15; DB 9; Length 112;
Best Local Similarity	100.0%; Pred. No. 1.1e+03;
Matches	15: conservative 0; Mismatches 0; Indels 0; Gaps 0;
0y	3 tagtagcagctctgcgc 17
Db	67 TAGTCACGCTTCGC 53
LOCUS	AV922948/C
DEFINITION	AV922948 168 bp mRNA linear EST 18-JAN-2002
KEYWORDS	leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA
ACCESSION	AV922948
VERSION	AV922948.1 GI:18218727
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare.
ORGANISM	Hordeum vulgare subsp. vulgare
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
TITLE	; Trilicaceae; Hordeum.
JOURNAL	1 (bases 1 to 168)
COMMENT	Sato, K., Saisho, D. and Takeda, K. Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002) Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp. Location/Qualifiers 1..168
FEATURES	/organism="Hordeum vulgare subsp. vulgare" source /cultivar="Haruna Nijo" /db_xref="taxon:112509"

BASE COUNT	36 a	56 c	49 g	27 t	
ORIGIN	/clone-"basd3b11" /clone_1lb-"K. Sato unpublished cDNA library, cv. Haruna Nijo second leaf stage seedling leaves" /tissue_type-"seedling leaves" /dev_stage-"second leaf stage"				
Query Match	83.3%	Score 15:	DB 9:	Length 168:	
Best Local Similarity	100.0%	Pred. No. 1.3e+03:			
Matches 15:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:	
Oy	3	tagtagcagcttcgc 17			
Db	111	TAGTCACGCTCTCC 97			
RESULT 12					
LOCUS	AA324668/C	241 bp	mRNA	linear	EST 20-APR-1997
DEFINITION	ES272818 Cerebellum II Homo sapiens cDNA 5' end, mRNA sequence.				
ACCESSION	AA324668				
VERSION	AA324668.1	GI:1977158			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 241)				
AUTHORS	Adams,M.D., Kerlavage,A.R., Fletschmann,R.D., Fudner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Whitecay,J.D., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodetz,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Smali,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y., F., Ming,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.				
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence				
JOURNAL	Nature 377 (6547 suppl), 3-174 (1995)				
MEDLINE	96026280				
COMMENT	Other_ESTs: THC190996 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hg1/hg1.html) Seq primer: M13 Reverse.				
FEATURES	Location/Qualifiers 1..241 /organism="Homo sapiens" /db_xref="ATCC (inhost):125407" /db_xref="taxon:9606" /clone_1lb="Cerebellum II" /tissue_type="cerebellum" /dev_stage="adult" /note="Organ: brain; Vector: pluescript SK-; site_1: EcoRI; site_2: XhoI"				

BASE COUNT 50 a 65 c 75 g 46 t 5 others
ORIGIN

Query Match 83.3%; Score 15; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 agtgcggtcgcgt 18
|||||
Db 223 AGTGCAGGTCTCGCT 209

RESULT 13
AA367189/c 256 bp mRNA linear EST 21-APR-1997
LOCUS EST78236 Pancreas tumor III Homo sapiens cDNA 5' end, mRNA
DEFINITION sequence.
ACCESSION AA367189
VERSION AA367189.1 GI:2019507
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 256)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodex,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nauyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinhe,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.M.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl.), 3-174 (1995)
COMMENT Other-ESTs: THC190996
Bioinformatics
Contact: Kerlavage, AR
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1..256
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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 agtgcggtcgcgt 18
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Db 117 AGTGCAGGTCTCGCT 103

RESULT 14
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LOCUS EST44299 Fetal brain I Homo sapiens cDNA 5' end, mRNA sequence.
DEFINITION sequence.
ACCESSION AA339193
VERSION AA339193.1 GI:1991472
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 276)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodex,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nauyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinhe,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.M.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
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MEDLINE Nature 377 (6547 Suppl.), 3-174 (1995)
COMMENT Other-ESTs: THC190996
Bioinformatics
Contact: Kerlavage, AR
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1..276
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Query Match 83.3%; Score 15; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 agtgcggtcgcgt 18
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Db 188 AGTGACGGTCTCGCT 174

RESULT 15
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DEFINITION	IL5-HT0009-180999-001-D12 HT0009 Homo sapiens CDNA, mRNA sequence.			

DEFINITION ILS-HT0009-180999-001-D12 HT0009 Homo sapiens cDNA, mRNA sequence.

DEFINITION ILS-HT0009-180999-001-D12 HT0009 Homo sapiens cDNA, mRNA sequence.

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VERSION AW351943.1 GI:6849656
KEYWORDS EST.

SOURCE human.

ORGANISM	Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 329)

AUTHORS
HCGP <http://www.ludwig.org.br/loresites>.

TITLE The FAPES/LICK Human Cancer Genome Project

JOURNAL
Unpublished (1999)
COMMENT: Simpson &

COMMENT
collat.: SIMPSON A.D.G.
Laboratory of Cancer Ge-

Ludwig Institute for Cancer Research

Rua Prof. Antônio Prudente 109, 4 andar

BR211

Tel: +55-11-27049222

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-HT0009->

180999-001-D12&t3=1999-09-18&t4=1)

FEATURES

Location/Qualifiers

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Site 2: Smat: A mini-library was made by cloning prod

ORSTES (ORSTES, U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

BASE COUNT	53 a	91 c	95 g	90 t
ORIGIN				

Query Match	83.38; Score 15; DB 9; Length 329;
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 agtgcggtctcgct 18

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DB 312 AGTGACGGTCTCGCT 326

Search completed: August 21, 2002, 21:32:20
Job time: 12519 sec

Job time: 12519 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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31.935 Million cell updates/sec

Title: US-10-046-955-49

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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27	14	77.8	1443	2	US-08-403-853-19

C 28	14	77.8	1446	4	US-09-171-945-130	Sequence 130, App
C 29	14	77.8	1572	1	US-08-353-400-23	Sequence 23, App1
C 30	14	77.8	1632	2	US-08-792-824-8	Sequence 8, App1
C 31	14	77.8	1641	1	US-08-792-824-5	Sequence 5, App1
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C 45	13.8	76.7	1270	5	PCT-US94-05288-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-08-652-127C-8
Sequence 8, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hameljin
TITLE OF INVENTION: DETECTION OF PLANT
TITLE OF INVENTION: PATOGEN FUNGI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
ADDRESS: Seaby & Maclean
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 583
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-8

Query Match 91.1% Score 16.4; DB 1; Length 583;
Best Local Similarity 94.4% Pred. No. 3.6;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tctagtgcgctcgcct 18
Db 429 TCTAGTGCCTCCT 446

```

RESULT 2
US-08-652-127C-5
: Sequence 5, Application US/08652127C
: Patent No. 5792611
: GENERAL INFORMATION:
: APPLICANT: Richard C. Hamelin
: TITLE OF INVENTION: DETECTION OF PLANT
: TITLE OF INVENTION: PATHOGEN FUNGI
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: George A. Seaby
: ADDRESSEE: Seaby & Maclean
: STREET: 880 Wellington Street, Suite 708
: CITY: Ottawa
: COUNTRY: Canada
: ZIP: K1R 6K7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/652.127C
: FILING DATE: May 23, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: George A. Seaby
: REGISTRATION NUMBER: 24,034
: REFERENCE/DOCKET NUMBER: 1898
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (613) 232-5815
: TELEFAX: (613) 232-5831
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 594
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-08-652-127C-5

Query Match 91.1%; Score 16.4; DB 1; Length 594;
Best Local Similarity 94.4%; Pred. No. 3.6;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 tctagtgaacggtctgcgt 18
||||| |||||||
DB 439 tctagtgcggtctgcgt 456

RESULT 3
US-09-645-073-1
: Sequence 1, Application US/09645073
: Patent No. 6287800
: GENERAL INFORMATION:
: APPLICANT: Lee, May
: APPLICANT: Galazzo, Jorge
: TITLE OF INVENTION: Production of High Titers of Glibdrellins GA4 and GA7
: FILE REFERENCE: L02-01NP
: CURRENT APPLICATION NUMBER: US/09/645,073
: CURRENT FILING DATE: 2000-08-25
: PRIOR APPLICATION NUMBER: US 60/151,770
: PRIOR FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 2293
: TYPE: DNA
: ORGANISM: Glibdrellia fujikuroi
: US-09-645-073-1

Query Match 91.1%; Score 16.4; DB 4; Length 2293;

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Best Local Similarity 94.4%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgct 18
      ||||| |||||
DB 2145 tctagtgcggtctcgct 2162

RESULT 4
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652.127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-652-127C-7

Query Match 82.2%; Score 14.8; DB 1; Length 531;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tctagtacggtctcgct 18
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DB 377 TATAGTGGCGGTCTCGCT 394

RESULT 5
US-08-652-127C-6
; Sequence 6, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: George A. Seaby
; ADDRESSEE: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
;

```

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 18:13:06 : Search time 2238.68 Seconds
(without alignments)
3411.915 Million cell updates/sec

Title: US-10-046-955-5

Perfect score: 365
Sequence: 1 aaacttcaacaatgatct.....gggatacccgctgaacttaa 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1:	gb_da:*
2:	gb_htg:*
3:	gb_ln:*
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9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_vl:*
15:	em_ba:*
16:	em_fun:*
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18:	em_in:*
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20:	em_om:*
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30:	em_htg_hum:*
31:	em_htg_inv:*
32:	em_htg_other:*
33:	em_htgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	365	100.0	365	8	ENU93686	U93686	Emeritella
2	334.8	91.7	560	8	EQJ000934	AF138289	Emeritella
3	334.8	91.7	565	8	AF138289	AF138289	Emeritella
4	327.6	89.8	561	8	EQJ000935	AJ000935	Emeritella
5	322.8	88.4	558	8	EQJ000931	AJ000931	Emeritella
6	318.8	87.3	496	8	EN1276063	AJ276063	Emeritella
7	316.4	86.7	563	8	EVJ000932	AJ000932	Emeritella
8	306.4	83.9	569	8	AF157507	AF157507	Aspergillus
9	304	83.3	549	8	AF261558	AF261558	Aspergillus
10	297.2	81.4	493	8	AF078899	AF078899	Emeritella
11	295.6	81.0	493	8	AF078898	AF078898	Emeritella
12	290.8	79.7	1148	8	AF033428	AF033428	Penicillium
13	288	78.9	581	8	AEU65310	U65310	Aspergillus
14	286.8	78.6	1110	8	AF033421	AF033422	Penicillium
15	286.8	78.6	1110	8	AF033422	AF033423	Penicillium
16	286.8	78.6	1110	8	AF033423	AF033424	Penicillium
17	285.4	78.2	566	8	EIJ000936	AJ000936	Emeritella
18	285.2	78.1	1144	8	AF033405	AF033405	Penicillium
19	284.2	77.9	365	8	ANU93685	AF033433	Penicillium
20	283.2	77.6	1144	8	AF033433	AF033457	Penicillium
21	282.8	77.5	1141	8	AF033457	AF028009	Aspergillus
22	281.6	77.2	579	8	AF028009	AF033425	Eupenicillium
23	281.4	77.1	1147	8	AF033425	AJ223852	Aspergillus
24	281	77.0	595	8	ANAJ3852	U65304	Aspergillus
25	280.6	76.9	1150	8	AH065304	AF138288	Aspergillus
26	279.8	76.7	596	8	AF138288	AF348420	Aspergillus
27	279.8	76.7	614	8	AF348420	AJ280013	Aspergillus
28	279	76.4	600	8	AHE280013	AF033441	Penicillium
29	278.4	76.3	1142	8	AF033441	AF078889	Aspergillus
30	278.2	76.2	597	8	AF078889	AF459733	Neosartoris
31	278.2	76.2	1189	8	AF459733	AF033492	Penicillium
32	278	76.2	1141	8	AF033492	AF033402	Penicillium
33	278	76.2	1143	8	AF033402	AF033434	Penicillium
34	277.6	76.1	1145	8	AF033434	AF033416	Penicillium
35	277.6	75.8	1144	8	AF033416	AF033427	Penicillium
36	276.8	75.8	1144	8	AF033427	AF125946	Penicillium
37	276.8	75.8	1144	8	AF125946	AF125937	Penicillium
38	276.4	75.7	1141	8	AF125937	AF048741	Verticillium
39	276.2	75.7	566	8	AF048741	AF033415	Penicillium
40	275.8	75.6	1144	8	AF033415	AF034462	Penicillium
41	275.8	75.6	1144	8	AF034462	AF033429	Penicillium
42	275.8	75.6	1150	8	AF033429	AF033419	Penicillium
43	275.6	75.5	1143	8	AF033419	AF033417	Penicillium
44	275.6	75.5	1144	8	AF033417	AF034463	Penicillium
45	275.6	75.5	1141	8	AF034463		

ALIGNMENTS

RESULT 1

ENU93686

LOCUS

DEFINITION

Emeritella nidulans 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, complete sequence, and 28S ribosomal RNA gene, partial sequence.

ACCESSION

U93686

VERSION

U93686.1

KEYWORDS

U93686

SOURCE

U93686.1

ORGANISM

Emeritella nidulans.

REFERENCE

1 (bases 1 to 365)

AUTHORS

De Aguiar, L.A., Vaisnav, H., Westerman, J.M., Reiss, E., Lott, T.J., and Mortison, C.J.

TITLE

Direct Submission

JOURNAL

Submitted (28-FEB-1997) Mycology, Centers for Disease Control and Prevention, 1600 Clifton Road, N.E., Atlanta, GA 30333, USA

FEATURES

source

1..365

/organism="Emeritella nidulans"

/db_xref="taxon:162425"

/note="CDC Mycological Reference Laboratory B5446"
rRNA
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 158..327
 /note="Internal transcribed spacer 2: ITS2"
rRNA
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 /product="28S ribosomal RNA"
BASE COUNT
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ORIGIN

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Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaattcaacaatgagatccttggtccgcatcgatgaagaacgacgacatcgat 60
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DB 1 AAACCTTCAACATGATCTCTGTTCCGCGATGATGAAGACGCGAATCGCAT 60
 |||||

QY 61 aagtaatgtaattgcaaatatcagatcatcagatcagatcagatcagatcagatc 120
 |||||
DB 61 AAGTAATGTGAATTCGAATTCAGTGAATCATGAGTCTTGAACGACATCGGCC 120
 |||||

QY 121 ctgagatccgagggagcagctcctcagagcagcagcagcagcagcagcagcagc 180
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DB 121 CTGAGATTCGGGGGGGAGTGCCTGTCCAGCGCTCATTCCTCCCAAGCCGGCTGTG 180
 |||||

QY 181 tgttgagtcgtcgtcccccgcggggagcggcgcaagagcggcgagcggcggtc 240
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DB 181 TGTTCGGTCTGTCCTCCCGCCCGGGGAGCGGCCCAAGAGCGCGACCGCTG 240
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QY 241 cggctcagagcgtatgggagcttgatcaccgctcagatgaagccggcgccagcc 300
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DB 241 CGGCTCTCGAGCGATGAGGGGCTTGTCACCCGCTGATTAAGCGCGCGCCGAC 300
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QY 301 ggcgtcccaacctatcttcctcaggtgacccgcagtcagtagagataccgcgtgaa 360
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DB 301 GCGCTCTCCAACTTATCTTCTCAGTTGACCTCGATCGATGAGTGGATACCGCTGAA 360
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QY 361 cttaa 365
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DB 361 CTTAA 365

RESULT 2
EOJ000934 560 bp DNA linear PLN 12-OCT-1998
LOCUS Emericella quadrillinea strain FMR 5966, 5.8S rRNA gene, ITS1 and ITS2.
DEFINITION

ACCESSION AJ000934
VERSION AJ000934.1 GI:3757579
KEYWORDS 5.8S rRNA gene; ITS1; ITS2.
SOURCE Emericella quadrillinea.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; Emericella.
REFERENCE
AUTHORS Cano,J.F.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1998) CANO J.F., UNITAT DE MICROBIOLOGIA,
 FACULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç
 21, Reus, 43201 - Reus - Tarragona, SPAIN
REFERENCE
AUTHORS Schigel,A., Cano,J. and Guarro,J.
TITLE A new species of Emericella and anomalous strains of
 E.quadrillinea
JOURNAL Unpublished
FEATURES
 source Location/Qualifiers
 1..560
 /organism="Emericella quadrillinea"
 /variety="gemmata"
 /strain="FMR 5966"
 /db_xref="taxon:41735"

/tissue_type="mycelium/hyphal"
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 /note="Internal transcribed spacer 1 (ITS1)"
rRNA
 183..339
 /gene="5.8S rRNA"
 /citation=[2]
 /product="5.8S ribosomal RNA"
gene
 183..339
 /gene="5.8S rRNA"
misc_feature
 340..560
 /note="Internal transcribed spacer 2 (ITS2)"
BASE COUNT 112 a 166 c 164 g 118 t
ORIGIN

Query Match
Best Local Similarity 91.7%; Score 334.8; DB 8; Length 560;
Matches 360; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

QY 1 aaattcaacaatgagatccttggtccgcatcgatgaagaacgacgacatcgat 60
 |||||
DB 183 AAACCTTCAACATGATCTCTGTTCCGCGATGATGAAGACGCGAATCGCAT 242
 |||||

QY 61 aagtaatgtaattgcaaatatcagatcatcagatcagatcagatcagatcagatc 120
 |||||
DB 243 AAGTAATGTGAATTCGAATTCAGTGAATCATGAGTCTTGAACGACATCGGCC 302
 |||||

QY 121 ctgagatccgagggagcagctcctcagagcagcagcagcagcagcagcagcagc 180
 |||||
DB 303 CTGAGATTCGGGGGGGAGTGCCTGTCCAGCGCTCATTCGCTTGAACCGCGCTTG 362
 |||||

QY 181 tgttgagtcgtcgtcccccgcggggagcggcgcaagagcggcgagcggcggtc 239
 |||||
DB 363 TGTTCGGTCTGCT---CCCCCGGGGAGAGCGGCCGAAAGCAGCGCGACCGTGT 419
 |||||

QY 240 cggctcagagcgtatgggagcttgatcaccgctcagatgaagccggcgccagcagc 299
 |||||
DB 420 CGGCTCTCGAGCGATGAGGGGCTTTCACCCGCTGATTAAGCGCGCGCCGAC 479
 |||||

QY 300 ggcgtcccaacctatcttcctcaggtgacccgcagtcagtagagataccgcgtgaa 359
 |||||
DB 480 GCGCTCTCCAACTTATCTTCTCAGTTGACCTCGATCGATGAGTGGATACCGCTGAA 539
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QY 360 actaa 365
 |||||
DB 540 ACTTAA 545

RESULT 3
AF138289 565 bp DNA linear PLN 11-APR-2000
LOCUS AF138289
DEFINITION Emericella nidulans 18S ribosomal RNA gene, partial sequence;
 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
ACCESSION AF138289
VERSION AF138289
KEYWORDS Aspergillus nidulans.
SOURCE Aspergillus nidulans.
ORGANISM Aspergillus nidulans.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; Emericella.
REFERENCE
AUTHORS Henry,T., Iwen,P.C. and Hinrichs,S.H.
TITLE Identification of Aspergillus species using internal transcribed
 spacer regions 1 and 2
JOURNAL J Clin. Microbiol. 38 (4), 1510-1515 (2000)
MEDLINE 20211684
PUBMED 10747135
REFERENCE
AUTHORS Henry,T.J., Iwen,P.C. and Hinrichs,S.H.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-1999) Pathology and Microbiology, University of

Nebraska Medical Center, 986495 Nebraska Medical Center, Omaha, NE
68198-6495, USA
Location/Qualifiers
1. .565
/organism="Aspergillus nidulans"
/strain="ATCC10074"
/db_xref="ATCC:10074"
/db_xref="taxon:5072"
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/product="18S ribosomal RNA"
31. .183
/product="Internal transcribed spacer 1"
184. .339
/product="5.8S ribosomal RNA"
340. .507
/product="Internal transcribed spacer 2"
508. .>565
/product="28S ribosomal RNA"

BASE COUNT 115 a 166 c 168 g 116 t
ORIGIN

Query Match 91.7%; Score 334.8; DB 8; Length 565;
Best Local Similarity 98.4%; Pred. No. 3.6e-64;
Matches 360; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

OY 1 aaacttcaacaatgagatctctgtgtccgcatcgaatgaagaacgacgacgacatgcgat 60
|||||
DB 183 AAACCTTCAACATGATGATCTGTTCCGGCATCGATGATGATGATGATGATGATGAT 242
OY 61 aagtaatgtaattgcagaatcagtgatcatcgaatcttgaacgacatgcgccc 120
|||||
DB 243 AACTAATGTAATTCAGATTCAGTAATTCAGATTCAGATTCAGATTCAGATTCAGATTC 302
OY 121 ctggcatccgggggacgacgctgtccgacgctcatctgtccctcaacccggcctgtg 180
|||||
DB 303 CTGGCATCTCGGGGGGACGATGCTGTCGAGCGTATGCTGCTCAACCGCGCTTGTG 362
OY 181 tgttggtcgtcgtcccccgggggacgagccggaagaacgacgacgacgacgacg-9t 239
|||||
DB 363 TGTGTGGTGGTGGT---CCGCCCGGGGAGACGGGCCGGAAGGACGCGGCGACCGTGT 419
OY 240 cgggtcccgacgagcgtatgggcttggtacacccgctcgtatgaagcggcgacgacgacg 299
|||||
DB 420 CCGGCTCTCGACGCGTATGGGGGCTTTGTCAACCGCTGATTAAGGGCGCGCGCGCCACAC 479
OY 300 cggcgtcccaacctatcttctcaggttgtaacctcgaatcgaatgaggaataccgctga 359
|||||
DB 480 CGGCGTCTCCAACTTATTTTCTCAGTTGACCTCGATCAGTACGATGAGGATACCGCTGA 539
OY 360 acttaa 365
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DB 540 ACTTAA 545

RESULT 4
EQJ000935 561 bp DNA linear PLN 14-OCT-1998
LOCUS Emericella quadrilineata strain IMI 371927, 5.8S rRNA gene, ITS1
DEFINITION and ITS2.
ACCESSION AJ000935
VERSION AJ000935.1 GI:3757580
KEYWORDS 5.8S rRNA gene; ITS1; ITS2.
SOURCE Emericella quadrilineata.
ORGANISM Emericella quadrilineata
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

REFERENCE
AUTHORS Cano, J.F.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1998) CANO J.F., UNITAT DE MICROBIOLOGIA,
FACULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç
21, Reus, 43201 - Reus - Tarragona, SPAIN

REFERENCE 2 (bases 1 to 561)
AUTHORS Stohiguel, A., Cano, J., and Guarro, J.
TITLE A new species of Emericella and anomalous strains of E.
quadrilineata
JOURNAL unpublished
FEATURES
source Location/Qualifiers
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/organism="Emericella quadrilineata"
/variety="gemmata"
/strain="IMI 371927"
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/rissue_type="mycelium/hyphal"
30. .181
/note="Internal transcribed spacer 1 (ITS1)"
182. .338
/gene="5.8S rRNA"
/product="5.8S ribosomal RNA"
182. .338
/gene="5.8S rRNA"
339. .561
/note="Internal transcribed spacer 2 (ITS2)"

BASE COUNT 112 a 166 c 164 g 119 t
ORIGIN

Query Match 89.8%; Score 327.6; DB 8; Length 561;
Best Local Similarity 97.0%; Pred. No. 1.4e-62;
Matches 355; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

OY 1 aaacttcaacaatgagatctctgtgtccgcatcgaatgaagaacgacgacgacatgcgat 60
|||||
DB 182 AAACCTTCAACATGATGATCTGTTCCGGCATCGATGATGATGATGATGATGATGAT 241
OY 61 aagtaatgtaattgcagaatcagtgatcatcgaatcttgaacgacatgcgccc 120
|||||
DB 242 AAGTATGTAATTCAGATTCAGTAATTCAGATTCAGATTCAGATTCAGATTCAGATTC 301
OY 121 ctggcatccgggggacgacgctgtccgacgctcatctgtccctcaacccggcctgtg 180
|||||
DB 302 CTGGCATCTCGGGGGGACGATGCTGTCGAGCGTATGCTGCTCAACCGCGGCGCT-7G 360
OY 181 tgttggtcgtcgtcccccgggggacgagccggaagaacgacgacgacgacg-9t 239
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DB 361 TGTGTGGTGGTGGTCCCGCGGGGAGCGGCCGGAAGGACGCGGCGACCGTGT 420
OY 240 cgggtcccgacgagcgtatgggcttggtacacccgctcgtatgaagcggcgacgacgacg 299
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DB 421 CCGGCTCTCGACGCGTATGGGGGCTTTGTCAACCGCTGATTAAGGGCGCGCGCGCCAGC 480
OY 300 cggcgtcccaacctatcttctcaggttgtaacctcgaatcgaatgaggaataccgctga 359
|||||
DB 481 CGGCGTCTCCAACTTATTTTCTCAGTTGACCTCGATCAGTACGATGAGGATACCGCTGA 540
OY 360 acttaa 365
|||||
DB 541 ACTTAA 546

RESULT 5
EQJ000931 558 bp DNA linear PLN 12-OCT-1998
LOCUS Emericella quadrilineata 5.8S rRNA gene, ITS1 and ITS2.
DEFINITION
ACCESSION AJ000931
VERSION AJ000931.1 GI:3757576
KEYWORDS 5.8S rRNA gene; ITS1; ITS2.
SOURCE Emericella quadrilineata.
ORGANISM Emericella quadrilineata
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.

REFERENCE
AUTHORS Cano, J.F.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1998) CANO J.F., UNITAT DE MICROBIOLOGIA.

	REFERENCE	PNCULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç
	AUTHORS	21. Reus, 43201 - Reus - Tarragona, SPAIN
	TITLE	2 (bases 1 to 558) Stichigel,A., Cano,J. and Guarro,J. A new species of Emericella and anomalous strains of E. quadralineata
JOURNAL	Unpublished	
FEATURES	Location/Qualifiers	
source	1..558 /organism="Emericella quadralineata" /isolate="soil, Australia" /strain="IMI 370017" /db_xref="taxon:41735" /lissue_type="mycelium/hyphal"	
misc_feature	30..181 /note="internal transcribed spacer 1 (ITS1)"	
rRNA	182..338 /gene="5.8S rRNA" /product="5.8S ribosomal RNA" 182..338 /gene="5.8S rRNA"	
gene	339..558 /note="internal transcribed spacer 2 (ITS2)"	
BASE COUNT	112 a 165 c 163 g 118 t	
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Query Match	88.4% Score 322.8; DB 8; Length 558;	
Best Local Similarity	98.1%; Pred. No. 1,6e-61;	
Matches	359; Conservative 0; Mismatches 2; Indels 5; Gaps 3;	
OY	1 aaacttcaacaatgagctccttggttcgcgcacgatgaagaacgcagcaactcgcat	60
Db	182 AAACCTTCAAAATGCATCTCTGTCCGCCATCGATGAAGAACGACGCAACTGCGAT	241
OY	61 aagaaatgtagattgcagaattcagtagatcatcgaatcgtttgaacgcacattggcccc	120
Db	242 AAGTAATGTGAATTGCACAATAATTCAGTAGAATCATCAGTCTTTGAACGCACATTGGCCCC	301
OY	121 ctggcattccggaggagcattgctctgcgcagcgatcattgctgccctcaaaccggattg	180
Db	302 CTGGCATTCGGGGGGGCGATGCTGCCGAGGGTCAATTGCTGCCCTCAAGCCCGGCTTG	361
OY	181 tgltggagctgcgtgcctcccctccggaggagggccgaagaaggcagcgcgacacg	239
Db	362 TGTTGCGTGTGTCG---CCCCCCCGGGGAGCGGCCCAAAGCACGCGCGCACCGTCT	418
OY	240 ccgagtcctcggagcgatatgggcttggtcacccgcgtcgaattagggcgcgcgccagc	299
Db	419 CCGGCTCCGAGCGATGGGGCTTTGTACCCGCGTCGATTAGGCGCGGCGCGCCAGC	478
OY	300 cgagcgtcccaaccttaaccttctcgaagtgtgacctggagtcagtagagataccgcgtga	359
Db	479 CGGCGCTCCCAACTTATTTTCTCAGGCTTGACCTCGGATCA-GTAAAGGATACC	537
OY	360 acttaa 365	
Db	538 ACTTAA 543	
RESULT	6	
LOCUS	ENI276063	
DEFINITION	Emericella nidulans 496 bp DNA linear PLN 09-AUG-2000	
ACCESSION	AJ276063.1 GI:7208819	
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; internal transcribed spacer 2; ITS1; ITS2.	
SOURCE	Aspergillus nidulans.	
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.	
REFERENCE	1 (bases 1 to 496)	

AUTHORS	Webb J.S., Nixon,M., Eastwood,I.M., Greenhalgh,M., Robson,G.D. and Handley,P.S.					
TITLE	Fungal colonization and biodeterioration of plasticized polyvinyl chloride					
JOURNAL	Appl. Environ. Microbiol. 66 (8), 3194-3200 (2000)					
MEDLINE	20378616					
REFERENCE	2 (bases 1 to 496)					
AUTHORS	Webb,J.S.					
TITLE	Direct Submission					
JOURNAL	Submitted (05-MAR-2000) Webb J.S., School of Biological Sciences, University of Manchester, Stopford Building, Oxford Road, Manchester M13 0DP, UNITED KINGDOM					
FEATURES						
source	1..496 Location/Qualifiers					
	/organism="Aspergillus nidulans"					
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	/db_xref="taxon:5072"					
	/country="United Kingdom"					
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misc_feature	/note="Isolated from plasticised PVC"					
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	/gene="5.8S rRNA"					
gene	/product="5.8S ribosomal RNA"					
	150..306					
	/gene="5.8S rRNA"					
misc_feature	307..496					
	/note="internal transcribed spacer 2, ITS2"					
BASE COUNT	92 a 151 c 150 g 103 t					
ORIGIN						
Query Match	87.3%; Score 318.8; DB 8; Length 496;					
Best Local Similarity	98.3%; Pred. No. 1.3e-60;					
Matches	344; Conservative 0; Mismatches 2; Indels 4; Gaps 2					
OY	1	aacttcacaatgatgcctcttggtgccgcatcagtaagaacgcgaactcgat	60			
Db	150	AAATCTTCAACATGAGTCATTGGTTCCGGCATGATGAAGAAGCAGCGAATCGAT	209			
OY	61	aagtaatgaattcagaattcaagtgaatacagtagcttgaacgacatigccccc	120			
Db	210	AAGTAATGTAAATTGCAGATTCAAGTAATCATCAGACTTTGAAGCACATTCGCCCC	269			
OY	121	ctggcattccgggggagcagtcgtctcgaagcgtcatctgacctcaagccggctgtg	180			
Db	270	CTGGCATTCGGGGGAGCATGCTGTCGAGCGTCAATCTGCGCTCAAGCCGGCTGTG	329			
OY	181	tgtttggttgtgtcccccccccccgaggagagcgccaaagagcagcggtgaccg	-gt 239			
Db	330	TGTTGGGTCTCTGT---CCCCCCCCGGGGACGGGCCCAAAGGACGCGCGCACCTGT	386			
OY	240	cgcgtccctcgaagcgtatgtagcttgcgtcacccgcctcgaattagggccggcggtccagc	299			
Db	387	CGGCTCTCGAGCGATGGGGCTTTGTCTACCCGCTCGATTAGGGCCGGCGGGCCAGC	446			
OY	300	cggcgtctccaacctatcttctcaaggtgaacctcgatcaggtagga	349			
Db	447	CGGGCTCTCCAACCTATTATTTTCTCAGGTGACCTCGGATCAGGTAGGA	496			
RESULT	7					
EJVD000932	EJVD000932					
LOCUS	EJVD000932 563 bp DNA linear PLN 12-OCT-1998					
DEFINITION	Emmericella variecolor 5.8S rRNA gene, ITS1 and ITS2.					
ACCESSION	AJ000932					
VERSION	AJ000932.1 GI:3757577					
KEYWORDS	5.8S rRNA gene; ITS1; ITS2.					
SOURCE	Emmericella variecolor					
ORGANISM	Emmericella variecolor					
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eufariales; Trichocomaceae; Emmericella.					

REFERENCE	1 (bases 1 to 563)
AUTHORS	Cano, J.F.
TITLE	Direct Submission
JOURNAL	Submitted (11-FEB-1998) CANO J.F., UNITAT DE MICROBIOLOGIA, FACULTAT DE MEDICINA, UNIVERSITAT ROVIRA I VIRGILI, C/ Sant Llorenç 21, Reus, 43201 - Reus - Tarragona, SPAIN
REFERENCE	2. (bases 1 to 563)
AUTHORS	Stechigel, A.; Cano, J. and Guarro, J.
TITLE	A new species of <i>Emericella</i> and anomalous strains of <i>E. quadrilineata</i>
JOURNAL	unpublished
FEATURES	Location/Qualifiers
source	1. .563 /organism="Emericella varicolor" /strain="IMI 343522" /db_xref="taxon:41726" /tissue_type="mycelium/hyphal" 30. .183 /note="internal transcribed spacer 1 (ITS1)"
misc_feature	184. .340 /gene="5.8S rRNA" /product="5.8S ribosomal RNA" 184. .340 /gene="5.8S rRNA" 341. .563 /note="internal transcribed spacer 2 (ITS2)"
gene	184. .340 /gene="5.8S rRNA"
misc_feature	341. .563 /note="internal transcribed spacer 2 (ITS2)"
BASE COUNT	115 a 163 c 163 g 122 t
ORIGIN	
Query Match	86.7%, Score 316.4; DB 8; Length 563;
Best Local Similarity	96.7%; Pred. NO. 4.2e-60;
Matches	356; Conservative 0; Mismatches 6; Indels 6; Gaps 3;
QY	1 aaacttcaacatgagctctcttggttcgcgagtcgatacgaacgcagcagactgcgat 60
DB	184 AAACCTTCAACATGATGATCTCTTGCTCCGGCATGATGACGACGACGACATGGCAT 243
QY	61 aagtaatgcaatlcgagaatcagtaacatcagtcagctttgaaagcacattgcgccc 120
DB	244 AAGTAATGCAATTCAGAAATTCAGTGAATCATCGATCTTTGAACGACACATTCGCGCCC 303
QY	121 ctgagcatccggggggagatgcctgcgcgaagcgtcaattgctgcgc- tcaagccggcttgt 179
DB	304 CTGGCATTTCCGGGGGGGAGCTGCTGTCGACGCTCATTTCTGCTTCAAGCCCGGCTTGT 363
QY	180 gtcgtcgggtcgtgcgtcccccgcggggggaagcggcccgaaagcgacggcgacc--g 237
DB	364 GTGTTGGTGGTCTGCT---CCCCCGGGGGAGCGGGCCGAAAGCAGCGGGCGCACCGTG 420
QY	238 gtcgcgctcgcgagcgatgagccttggtgtacccgctcgatlaagggccggcgcgcca 297
DB	421 TCCCGATTCCTCCAGCGTAAGGGGCTTTGTACACCCGCTCATTAAGGCCGCGCGGCCCA 480
QY	298 gccgcgagctcgaaccttaattcttcacggttgacctcgatcaggtlaagatlaaccgct 357
DB	481 GCCGCGCTCCCAACCTTATTTTCTCAGAGTTGACCTCGATCAGTAGGATACCGGCT 540
QY	358 gaacttaa 365
DB	541 GAACCTTAA 548
RESULT	8
LOCUS	AF157507 569 bp DNA linear PLN 11-APR-2000
DEFINITION	<i>Aspergillus ustus</i> 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF157507
VERSION	AF157507.1 GI:5163469
KEYWORDS	

SOURCE	Aspergillus ustus.
ORGANISM	Aspergillus ustus.
REFERENCE	Eukaryotes: Fungi; Ascomycota: Pezizomycotina; Eurotiomycetes;
AUTHORS	Henriksen, T., Iwen, P.C. and Hinrichs, S.H.
TITLE	Identification of Aspergillus species using internal transcribed spacer regions 1 and 2
JOURNAL	J. Clin. Microbiol. 38 (4), 1510-1515 (2000)
MEDLINE	20211684
PUBMED	10747135
REFERENCE	2 (bases 1 to 569)
AUTHORS	Henry, T., Iwen, P.C. and Hinrichs, S.H.
TITLE	Direct Submission
JOURNAL	Submitted (08-JUN-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986495 Nebraska Medical Center, Omaha, NE 68198-6495, Douglas
FEATURES	Location/Qualifiers
source	1..569
	/organism="Aspergillus ustus"
	/db_xref="taxon:40382"
	/country="Canada: Alberta"
rRNA	<1..30
misc_RNA	/product="18S ribosomal RNA"
rRNA	31..186
	/product="internal transcribed spacer 1"
rRNA	187..342
misc_RNA	/product="5.8S ribosomal RNA"
rRNA	343..512
	/product="internal transcribed spacer 2"
rRNA	513..>569
	/product="28S ribosomal RNA"
BASE COUNT	113 a 167 c 164 g 125 t
ORIGIN	
Query Match	83.9% Score 306.4; DB 8; Length 569;
Best Local Similarity	96.7%; Pred. No. 6.9e-58;
Matches 356; Conservative	0; Mismatches 6; Indels 6; Gaps 4;
OY	1 aaacttcaacatgatctcttggttcgcggcatcgaataagaaacgcagaactcgat 60
DB	185 AAACCTTCAACAATGAGATCTTGTTCCGGCATCGATGAAGAAGCAGCAACTGCAT 244
OY	61 aagtaattgaattcagaaatcagtaaatcagtagctttgaaagcacatttgccccc 120
DB	245 AAGTAATGTGAATTCCAATAATCACTGATGATATCAAGCTTTGAAGCAGCATTCGCCCCC 304
OY	121 ctggcatcccgaggggcagtgcctgctcgagcgtcaatctgctgcc- tcaagccgagctgt 179
DB	305 CTGGCATTCGGGGGGGAGCATGCTGTCCAGAGCTCATTTGCTGCCCTTCAAGCCGGCTTGT 364
OY	180 gtgttggtgctgctgcctcccccccgaggggagaccgaaagcagcgcgagcag- g 238
DB	365 GTGTGGGGGTGCTGCT---CCCCCTCGGGGGAGAGGGCCCGAAGGACAGCGCGCACCGCG 421
OY	239 tcgcgttcctccgagcgtatgaggctctggttcaaccgcgctcgaattagggcgcggcgccag 298
DB	422 TCCGGTCTCCGAGCGGTATGCGGCTTTGTACACCCTCTCATTTAGGGCCGGCGGGCCAG 481
OY	299 ccgagcgtctccaaccttat-cttctcagagttgacctcgatcaggtcaggtacggtaccgct 357
DB	482 CCGGCGCTCCAAACCTTTATTTTACCAAGTTGACCTCGATCAGGTAGGGATTACCGCT 541
OY	358 gaacttaa 365
DB	542 GAACCTTAA 549
RESULT	9
AF261658	AF261658
LOCUS	549 bp DNA linear PLN 02-MAY-2001
DEFINITION	Aspergillus sp. GI306 small subunit ribosomal RNA gene, partial


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QY 240 ccggtcctcgcagcgtatgaggtcgtgacccgcgtcattgagcgccgagcgccagc 299
      |||
Db 398 CCGGCTCTCGAGCGATGATGGCGCTTGTGACCCGCTCGATTAAGCGCGCGGCGCCACC 457
      |||

QY 300 cggcgctcccaacctatctcttccaggtt 329
      |||
Db 458 CGGCTCTCGAACCTATTATTTCTCAGGTT 487
      |||

RESULT 11
AF078898 493 bp DNA linear PLN 11-JUN-2001
LOCUS AF078898
DEFINITION Emeritella nidulans environmental isolate C0095 18S ribosomal RNA
            gene, partial sequence; internal transcribed spacer 1, 5.85
            ribosomal RNA gene and internal transcribed spacer 2, complete
            sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF078898
VERSION AF078898.1 GI:4092047
KEYWORDS
SOURCE
ORGANISM Aspergillus nidulans.
            Aspergillus nidulans
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; Emeritella.
REFERENCE
AUTHORS 1 (bases 1 to 493)
            Zhao, J., Kong, F., Li, R., Wang, X., Wan, Z. and Wang, D.
TITLE Identification of Aspergillus fumigatus and related species by
            Nested PCR Targeting Ribosomal DNA Internal Transcribed Spacer
            Regions
JOURNAL J. Clin. Microbiol. 39 (6), 2261-2266 (2001)
PUBMED 11376067
REFERENCE 2 (bases 1 to 493)
            Kong, F., Li, R., Luo, Z. and Wang, D.
AUTHORS Phylogenetic Analysis of Pathogenic Aspergillus
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 493)
            Luo, Z., Li, R., Kong, F., Li, D., Yoshikazu, H. and Wang, D.
AUTHORS Direct Submission
TITLE Submitted (17-JUL-1998) Dermatology, First Hospital of Beijing
JOURNAL Medical University, Xishiku St., Beijing 100034, China
FEATURES
source 1. 493
            /organism="Aspergillus nidulans"
            /isolate="environmental isolate C0095"
            /db_xref="taxon:5072"
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            8..160
            /note="ITS1"
            /product="Internal transcribed spacer 1"
            161..317
            /product="5.8S ribosomal RNA"
            318..485
            /note="ITS2"
            /product="Internal transcribed spacer 2"
            486..>493
            /product="28S ribosomal RNA"
            93 a 152 c 142 g 106 t
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ORIGIN
Query Match 81.0%; Score 295.6; DB 8; Length 493;
Best Local Similarity 97.6%; Pred. No. 1.7e-55;
Matches 322; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

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QY 121 ctggcattccgggggycatgctgtctcgcagcgctcatctgtccctcaagcccgctgtg 180
      |||
Db 281 CTGGCATTCGGGGGGGCGATGCTGTCGAGCGCTCATTTGCTGCCCTCAACCGGGCTTGTG 340
      |||

QY 181 tgttggctcgtctcccccgcgggggacgggcccgaagagcagcgcgacccg 239
      |||
Db 341 TGTTGGTCTGCTGT---CCGCCCGGGGGGACGGGCCGAAGGACACGGCGACCGTGT 397
      |||

QY 240 ccggtcctcgcagcgtatgaggtcgtgacccgcgtcattgagcgccgagcgccagc 299
      |||
Db 398 CCGGCTCTCGAGCGATGATGGCGCTTGTGACCCGCTCGATTAAGCGCGCGGCGCCACC 457
      |||

RESULT 12
AF033428 1148 bp DNA linear PLN 13-FEB-2001
LOCUS AF033428
DEFINITION Penicillium implicatum strain NRRL 2061 internal transcribed spacer
            1, 5.8S ribosomal RNA gene and internal transcribed spacer 2,
            complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF033428
VERSION AF033428.1 GI:2668668
KEYWORDS
SOURCE
ORGANISM Penicillium implicatum.
            Penicillium implicatum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE
AUTHORS 1 (bases 1 to 1148)
            Peterson, S.W.
TITLE LSU-rDNA nucleotide sequences of Penicillium species based on ITS and
            LSU-rDNA nucleotide sequences
JOURNAL (in) Samson, R.A. and Pitt, J.I. (Eds.):
            INTEGRATION OF MODERN TAXONOMIC METHODS FOR PENICILLIUM AND
            ASPERGILLUS CLASSIFICATION: 163-178;
            Harwood Academic Publishers, The Netherlands (2000)
REFERENCE 2 (bases 1 to 1148)
            Peterson, S.W.
AUTHORS Phylogenetic analysis of Penicillium species based on ITS and
TITLE 18S-rDNA nucleotide sequences
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1148)
            Peterson, S.W.
AUTHORS Direct Submission
TITLE Submitted (07-NOV-1997) Microbial Properties Research, National
JOURNAL Center for Agricultural Utilization Research, 1815 N. University
            St., Peoria, IL 61604, USA
FEATURES
source 1. 1148
            /organism="Penicillium implicatum"
            /strain="NRRL 2061"
            /db_xref="taxon:69775"
            1..187
            /product="Internal transcribed spacer 1"
            188..344
            /product="5.8S"
            345..514
            /product="Internal transcribed spacer 2"
            515..>1148
            /product="28S"
            237 a 338 c 360 g 213 t
BASE COUNT
ORIGIN
Query Match 79.7%; Score 290.8; DB 8; Length 1148;
Best Local Similarity 92.4%; Pred. No. 1.8e-54;
Matches 340; Conservative 0; Mismatches 22; Indels 6; Gaps 3;

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ORIGIN

Query Match 78.6%; Score 286.8; DB 8; Length 1110;
Best Local Similarity 91.8%; Pred. No. 1.4e-53;
Matches 336; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

QY 1 aaacttcaacaatgatctcttggtccgcatcgaatgaagaacgacgaactgcgat 60
DB 151 AAACCTTCAACAGGATCTCTGTTCCGGCATGATGAAGACGACGAATGCGAT 210
QY 61 aagtaatgtaattgcgaattcagtaatacatgaatccttgaacacatcgcgcc 120
DB 211 AACTTAATGTGAATTCAGAAATTCAGTGAATATGAGCTTTGTAACGACATTCGCCCT 270
QY 121 ctggcaatccgaggggagcctgtccgagcgtatcgtcgtccccaagcccgctgtg 180
DB 271 CTGGTATTCGGAGGCGATGCTGTCCGAGCGTCATTCCTCCCTCAAGCCCGGCTTGTG 330
QY 181 tgttggtcgtcgtcccccgcgggggagcgccgaaagcagcgcgccgcg-gt 239
DB 331 TGTGGGGCCCGTCCCGCCGGGGAGCGGCCCGAAAGGACGCGCGCCGCGT 390
QY 240 ccggtccctcgaagcgtatgagcgtcgtccgagcgtcgtcgtccccaagcccgctgtg 299
DB 391 CCGGTCTCGAGCGATGAGGCGCTTCGTACCCGCTCTAGTAGGCCCGGCC-GGCGCCAGC 449
QY 300 cggcgtctccaacttacttctcgaagtgacctcgatcaggtagggataccgcgtga 359
DB 450 CGAC-CCCCAACCTTAAATATCTCAGGTGATCGATCAGTACGATAGGATACCCGCTGA 508
QY 360 acttaa 365
DB 509 ACTTAA 514

RESULT 15
AF033422 1110 bp DNA Linear PLN 13-FEB-2001
LOCUS AF033422
DEFINITION Penicillium citrinum strain NRRL 1841 internal transcribed spacer
1, 5.8S ribosomal RNA gene and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF033422
VERSION AF033422.1 GI:2668662
KEYWORDS
SOURCE Penicillium citrinum.
ORGANISM Penicillium citrinum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE
AUTHORS Peterson,S.W.
TITLE Phylogenetic analysis of Penicillium species based on ITS and
LSU-rDNA nucleotide sequences
JOURNAL (in) Samson,R.A. and Pitt,J.I. (Eds.):
INTEGRATION OF MODERN TAXONOMIC METHODS FOR PENICILLIUM AND
ASPERGILLUS CLASSIFICATION: 163-178;
Hartwood Academic Publishers, The Netherlands (2000)
REFERENCE
AUTHORS Peterson,S.W.
TITLE Phylogenetic analysis of Penicillium species based on ITS and
lsu-rDNA nucleotide sequences
JOURNAL Unpublished
REFERENCE
AUTHORS Peterson,S.W.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1997) Microbial Properties Research, National
Center for Agricultural Utilization Research, 1815 N. University
St., Peoria, IL 61604, USA
FEATURES
Source 1. 1110
Location/Qualifiers
/organism="Penicillium citrinum"
/strain="NRRL 1841"
/db_xref="taxon:5077"

misc_RNA 1..150
RNA /product="Internal transcribed spacer 1"
151..307
misc_RNA /product="5.8S"
308..476
RNA /product="Internal transcribed spacer 2"
477..>1110
BASE COUNT 241 a 313 c 338 g 218 t
ORIGIN

Query Match 78.6%; Score 286.8; DB 8; Length 1110;
Best Local Similarity 91.8%; Pred. No. 1.4e-53;
Matches 336; Conservative 0; Mismatches 27; Indels 3; Gaps 3;

QY 1 aaacttcaacaatgatctcttggtccgcatcgaatgaagaacgacgaactgcgat 60
DB 151 AAACCTTCAACAGGATCTCTGTTCCGGCATGATGAAGACGACGAATGCGAT 210
QY 61 aagtaatgtaattgcgaattcagtaatacatgaatccttgaacacatcgcgcc 120
DB 211 AACTTAATGTGAATTCAGAAATTCAGTGAATATGAGCTTTGTAACGACATTCGCCCT 270
QY 121 ctggcaatccgaggggagcctgtccgagcgtcgtcgtccccaagcccgctgtg 180
DB 271 CTGGTATTCGGAGGCGATGCTGTCCGAGCGTCATTCCTCCCTCAAGCCCGGCTTGTG 330
QY 181 tgttggtcgtcgtcccccgcgggggagcgccgaaagcagcgcgccgcg-gt 239
DB 331 TGTGGGGCCCGTCCCGCCGGGGAGCGGCCCGAAAGGACGCGCGCCGCGT 390
QY 240 ccggtccctcgaagcgtatgagcgtcgtccgagcgtcgtcgtccccaagcccgctgtg 299
DB 391 CCGGTCTCGAGCGATGAGGCGCTTCGTACCCGCTCTAGTAGGCCCGGCC-GGCGCCAGC 449
QY 300 cggcgtctccaacttacttctcgaagtgacctcgatcaggtagggataccgcgtga 359
DB 450 CGAC-CCCCAACCTTAAATATCTCAGGTGATCGATCAGTACGATAGGATACCCGCTGA 508
QY 360 acttaa 365
DB 509 ACTTAA 514

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 20:46:20 ; Search time 594.49 Seconds
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Title: US-10-046-955-5

Perfect score: 365
Sequence: 1 aaacttcacatgatcatc.....gggataccgcgtgaactaa 365

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapept 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	365	100.0	365	20	AAV70849	Sequence containin
2	284.2	77.9	365	20	AAV70847	Sequence containin
3	258.8	70.9	364	20	AAV70846	Sequence containin
4	256	70.1	556	20	AA222438	Infernal Transcrib
5	230.4	63.1	355	20	AAV70848	Sequence containin
6	221.2	60.6	382	21	AAV72782	5.8s rRNA gene seq
7	220.6	60.4	498	20	AA222437	Internal Transcrib
8	206.8	56.7	610	20	AA290111	Phomopsis viticola
9	206.6	56.6	309	20	AAV70872	Internal Transcrib

10	203.8	55.8	568	20	AA290112	Diplodia gossypina
11	195.2	53.5	640	22	AAH73767	Guillardia citrica
12	188.4	51.6	608	20	AA290110	Phomopsis viticola
13	184	50.4	618	22	AAH73768	Guillardia citrica
14	180.6	49.5	597	19	AAV43265	Sequence of ITS re
15	180.2	49.4	561	19	AAV59009	F. avenaceum Inter
16	179.4	49.2	553	21	AA291726	Rosellinia necatri
17	179.2	49.1	582	18	AA265100	T. harzianum IMI 3
18	177.8	48.7	549	21	AA291723	Rosellinia necatri
19	177.8	48.7	549	21	AA291724	Rosellinia necatri
20	176	48.2	537	21	AA291725	Rosellinia necatri
21	174.4	47.8	590	20	AA211797	DNA sequence of IT
22	171.8	47.1	615	22	AA211785	Consensus DNA sequ
23	171	46.8	2293	23	AA216211	Fungus genomic DNA
24	170.4	46.7	579	20	AA211794	DNA sequence of IT
25	170	46.6	569	18	AA265101	T. harzianum IMI 3
26	169.6	46.5	580	20	AA211793	DNA sequence of IT
27	169.4	46.4	578	24	ABA01155	Deuteromycetes pol
28	169.2	46.4	579	20	AA211785	Consensus DNA sequ
29	169.2	46.4	579	20	AA211786	DNA sequence of IT
30	169.2	46.4	579	20	AA211790	DNA sequence of IT
31	169.2	46.4	579	20	AA211792	DNA sequence of IT
32	169.2	46.4	579	22	AA211788	Internal Transcrib
33	168.8	46.2	579	20	AA211796	DNA sequence of IT
34	168	46.0	580	20	AA211796	Microdochium nival
35	167.6	45.9	545	16	AA205403	DNA sequence of IT
36	167.2	45.8	579	20	AA211787	DNA sequence of IT
37	166.8	45.7	588	19	AAV43267	Sequence of ITS re
38	166.6	45.6	580	20	AA211789	DNA sequence of IT
39	166.4	45.6	588	19	AAV43266	Sequence of ITS re
40	165.8	45.4	548	16	AA205394	Septoria tritici 1
41	165.8	45.4	548	19	AA205394	Septoria tritici 1
42	165.8	45.4	548	22	AA205394	Septoria tritici 1
43	165.6	45.4	556	19	AAV59008	Internal Transcrib
44	165.6	45.4	556	19	AAV62594	M. nivale Internal
45	165.4	45.3	626	16	AA205396	Microdochium nival

ALIGNMENTS

AAV70849	1	AAV70849 standard; DNA; 365 BP.
ID	AAV70849	standard; DNA; 365 BP.
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AC	AAV70849	
XX	AAV70849	
DT	26-FEB-1999	(first entry)
XX	26-FEB-1999	(first entry)
DE	Sequence containing the rDNA Internal transcribed spacer 2 (ITS2).	
XX	Sequence containing the rDNA Internal transcribed spacer 2 (ITS2).	
KW	5.8S ribosomal RNA gene; Internal transcribed spacer 2; ITS2;	
KW	28S ribosomal RNA gene; Probe: Aspergillus flavus; A. fumigatus;	
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;	
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus;	
KW	M. circinellioides f. circinellioides; Rhizopus oryzae; R. microsporus;	
KW	R. circinellioides f. stolonifer; Rhizomucor pusillus; Absidia corymbifera;	
KW	Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;	
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.	
XX	Aspergillus nidulans.	
OS	Aspergillus nidulans.	
XX	Aspergillus nidulans.	
PN	WO9805084-A2.	
XX	WO9805084-A2.	
PD	12-NOV-1998.	
XX	12-NOV-1998.	
PF	01-MAY-1998;	98WO-US089926.
XX	01-MAY-1998;	98WO-US089926.
PR	02-MAY-1997;	97US-0045400.
XX	02-MAY-1997;	97US-0045400.
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Aldorevich L, Choi JS, Morrison CJ, Reiss E;	

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XX
DR   WPI; 1999-034737/03.
XX
PT   New nucleic acid probes for filamentous fungi - for detecting e.g.
PT   Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT   Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT   species.
XX
PS   Claim 1; Page 11; 45pp; English.
XX
CC   The present sequence represents a partial 5.8S ribosomal RNA gene,
CC   internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
CC   gene. Probes can be derived from the present sequence which are
CC   species-specific. The specification also describes ITS2 sequence-derived
CC   probes for identifying a species selected from Aspergillus flavus,
CC   A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani,
CC   F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus,
CC   M. circinalis, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera,
CC   Cunninghamella elegans, Pseudallescheria boydii (teleomorph of
CC   Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenckii.
CC   The probes can be used for differentiating filamentous fungal species
CC   from each other and from other medically important fungi.
XX
SQ   Sequence 365 BP; 68 A; 109 C; 109 G; 79 T; 0 other:

Query Match      100.0%; Score 365; DB 20; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.1e-99;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY   1 aaacttcaacaatgatgattcttctggttcgagcatgatgaagaacgacgcaactcgat 60
DB   1 aaacttcaacaatgatgattcttctggttcgagcatgatgaagaacgacgcaactcgat 60
OY   61 aagtaagtgaatgacgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatc 120
DB   61 aagtaagtgaatgacgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatc 120
OY   121 ctggcattccgggggagcagtcgctgcgagcgcgcatgctgcgcctcaagccgctgtg 180
DB   121 ctggcattccgggggagcagtcgctgcgagcgcgcatgctgcgcctcaagccgctgtg 180
OY   181 tgttggtcgtctgtcccccgcgggggagcgggcccgaagcagcgcgacccgctc 240
DB   181 tgttggtcgtctgtcccccgcgggggagcgggcccgaagcagcgcgacccgctc 240
OY   241 cggctcccgagcgatgagggctgtgtaaccgctcgattagggccgagcgagccagcc 300
DB   241 cggctcccgagcgatgagggctgtgtaaccgctcgattagggccgagcgagccagcc 300
OY   301 ggcgtctcaaaccttattcttcaaggttgacctcgatcaggtaggtatgatacccgctgaa 360
DB   301 ggcgtctcaaaccttattcttcaaggttgacctcgatcaggtaggtatgatacccgctgaa 360
OY   361 cttaa 365
DB   361 cttaa 365

RESULT 2
ID   AAV70847 standard; DNA; 365 BP.
AC   AAV70847:
XX
DT   26-FEB-1999 (first entry)
XX
DE   Sequence containing the rDNA internal transcribed spacer 2 (ITS2).
XX
KM   5.8S ribosomal RNA gene; internal transcribed spacer 2; ITS2;
KM   28S ribosomal RNA gene; probe; Aspergillus flavus; A. fumigatus;
KM   A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;

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KM   Mucor rouxii; M. racemosus; M. plumbeus; M. indicus;
KM   M. circinalis; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KM   Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KM   Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX
OS   Aspergillus niger.
XX
PN   WO9850584-A2.
XX
PD   12-NOV-1998.
XX
PF   01-MAY-1998; 98WO-US08926.
XX
PR   02-MAY-1997; 97US-0045400.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Aldorevich L, Choi JS, Morrison CJ, Reis E;
XX
DR   WPI; 1999-034737/03.
XX
PT   New nucleic acid probes for filamentous fungi - for detecting e.g.
PT   Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT   Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT   species.
XX
PS   Claim 1; Page 10-11; 45pp; English.
XX
CC   The present sequence represents a partial 5.8S ribosomal RNA gene,
CC   internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
CC   gene. Probes can be derived from the present sequence which are
CC   species-specific. The specification also describes ITS2 sequence-derived
CC   probes for identifying a species selected from Aspergillus flavus,
CC   A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani,
CC   F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus,
CC   M. circinalis, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera,
CC   Cunninghamella elegans, Pseudallescheria boydii (teleomorph of
CC   Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenckii.
CC   The probes can be used for differentiating filamentous fungal species
CC   from each other and from other medically important fungi.
XX
SQ   Sequence 365 BP; 71 A; 106 C; 103 G; 85 T; 0 other:

Query Match      77.9%; Score 284.2; DB 20; Length 365;
Best Local Similarity 91.3%; Pred. No. 1.8e-75;
Matches 335; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

OY   1 aaacttcaacaatgatgattcttctggttcgagcatgatgaagaacgacgcaactcgat 60
DB   1 aaacttcaacaatgatgattcttctggttcgagcatgatgaagaacgacgcaactcgat 60
OY   61 aagtaagtgaatgacgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatc 120
DB   61 aagtaagtgaatgacgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatc 120
OY   121 ctggcattccgggggagcagtcgctgcgagcgcgcatgctgcgcctcaagccgctgtg 180
DB   121 ctggcattccgggggagcagtcgctgcgagcgcgcatgctgcgcctcaagccgctgtg 180
OY   181 tgttggtcgtctgtcccccgcgggggagcgggcccgaagcagcgcgacccgctc 240
DB   181 tgttggtcgtctgtcccccgcgggggagcgggcccgaagcagcgcgacccgctc 240
OY   241 tccggtctcgagcgatgagggctgtgtaaccgctcgattagggccgagcgagccag 298
DB   241 tccggtctcgagcgatgagggctgtgtaaccgctcgattagggccgagcgagccag 298
OY   299 ccgaggtctcaaaccttattcttcaaggttgacctcgatcaggtaggtatgatacccgctg 358
DB   299 ccgaggtctcaaaccttattcttcaaggttgacctcgatcaggtaggtatgatacccgctg 358

```

Oy 359 aacttaa 365
Db 359 aacttaa 365

RESULT 3

ID AAV70846 standard; DNA; 364 BP.

AAV70846;

26-FEB-1999 (first entry)

Sequence containing the rDNA Internal transcribed spacer 2 (ITS2).

5.8S ribosomal RNA gene; internal transcribed spacer 2; ITS2;
28S ribosomal RNA gene; probe; *Aspergillus flavus*; *A. fumigatus*;
A. niger; *A. terreus*; *A. nidulans*; *Fusarium solani*; *F. moniliforme*;
Mucor rouxii; *M. racemosus*; *M. plumbeus*; *M. indicus*;
M. circinelloides f. *circinelloides*; *Rhizopus oryzae*; *R. microsporus*;
R. circinans; *R. stolonifer*; *Rhizomucor pusillus*; *Ascidia corymbifera*;
Cunninghamella elegans; *Pseudallescheria boydii*; *Scedosporium apiospermum*;
Penicillium notatum; *Sporothrix schenckii*; filamentous fungus; ss.

Aspergillus fumigatus.

WO9650584-A2.

12-NOV-1998.

01-MAY-1998: 98WO-US08926.

02-MAY-1997: 97US-0045400.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Aldorevich L, Choi JS, Morrison CJ, Reiss E;

WPI: 1999-034737/03.

New nucleic acid probes for filamentous fungi - for detecting e.g.

Aspergillus, *Fusarium*, *Mucor*, *Rhizopus*, *Rhizomucor*, *Ascidia*.

Cunninghamella, *Pseudallescheria boydii*, *Penicillium* and *Sporothrix*

species.

Claim 1: Page 10: 45pp; English.

The present sequence represents a partial 5.8S ribosomal RNA gene,
internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
gene. Probes can be derived from the present sequence which are
species-specific. The specification also describes ITS2 sequence-derived
probes for identifying a species selected from *Aspergillus flavus*,
A. fumigatus, *A. niger*, *A. terreus*, *A. nidulans*, *Fusarium solani*,
F. moniliforme, *Mucor rouxii*, *M. racemosus*, *M. plumbeus*, *M. indicus*,
M. circinelloides f. *circinelloides*, *Rhizopus oryzae*, *R. microsporus*,
R. circinans, *R. stolonifer*, *Rhizomucor pusillus*, *Ascidia corymbifera*,
Cunninghamella elegans, *Pseudallescheria boydii* (teleomorph of
Scedosporium apiospermum), *Penicillium notatum*, or *Sporothrix schenckii*.
The probes can be used for differentiating filamentous fungal species
from each other and from other medically important fungi.

Sequence 364 BP: 74 A; 107 C; 102 G; 81 T; 0 other;

Query Match 70.9%; Score 258.8; DB 20; Length 364;
Best Local Similarity 90.5%; Pred. No. 7.3e-68;
Matches 333; Conservative 0; Mismatches 27; Indels 8; Gaps 5;

Oy 1 aaacttcaacatgatctcttggttcgcgatcgatgaagaacgcgcgaactgcgat 60
Db 1 aaacttcaacatgatctcttggttcgcgatcgatgaagaacgcgcgaactgcgat 60

Oy 61 aagtaatgtgaattgcagaattcagatcatcatcagatccttgcagcgaacttgcgcc 120
Db 61 aactaatgtgaattgcagaattcagatcatcatcagatccttgcagcgaacttgcgcc 120
Oy 121 ctggcattccggggggaactgccttcaggatcattgctgcgcc-tcaagccggcttgc 179
Db 121 ctggtatctccggggggaactgccttcaggatcattgctgcgcc-tcaagcagcgttgc 180
Oy 180 gtgttggttcgtctccccc-ccccgcgggagccgcggaagcagcgcgcgcacgcg- 237
Db 181 gtgttggttcgtctccccc-ccccgcgggagccgcggaagcagcgcgcgcacgcg- 240
Oy 238 gtccggtccctcagcgtatgggcttgcaccgcctcagatcaggcgcgcgcgcga 297
Db 241 gtccggtccctcagcgtatgggcttgcaccgcctcagatcaggcgcgcgcgcga 297
Oy 298 gccgcgcctcaccattatcttctcaggttgcaccgcctcagatcaggatgataccgct 357
Db 298 gccgcgc--accacattatcttctcaggttgcaccgcctcagatcaggatgataccgct 355
Oy 358 gaacttaa 365
Db 356 gaacttaa 363

RESULT 4

AA222438

AA222438;

02-DEC-1999 (first entry)

Internal Transcribed Spacer of *P. expansum*.

Internal Transcribed Spacer: ITS; fungus; yeast; fermentation; assay;

PCR; microorganism; wine-making; commercial; ds.

Penicillium expansum.

WO9946405-A1.

16-SEP-1999.

11-MAR-1999: 99WO-US004251.

11-MAR-1998: 98US-0037990.

(GALL-) GALLO WINERY E & J.

Engel SR, Descenzo RA, Morenzoni RA, Irelan NA;

WPI: 1999-551425/46.

New isolated fungal and yeast nucleic acids, used for identifying

different fermentation-related microorganisms, particularly in wine

fermentation cultures.

Disclosure: Page 32-33; 52pp; English.

This is the nucleotide sequence for the Internal Transcribed Spacer
(ITS) of *P. expansum*. This sequence was amplified directly from the
isolate by the ITS5 (AA222530) and ITS4 (22531) primers.
This invention is directed to the identification of different
fermentation-related microorganisms, particularly those involved in the
production of wine. The invention utilizes a polymerase chain reaction
(PCR) based diagnostic assay of DNA sequences located in the Internal
Transcribed Spacer (ITS) region of the ribosomal RNA gene.
Ribosomal genes are suitable for use as molecular probe targets because
of their high copy number. Non transcribed and transcribed spacer
sequences associated with ribosomal genes are usually poorly conserved
and, thus, are advantageously used as target sequences for the detection
of recent evolutionary divergence. Fungal RNA genes are organized in

CC units. Each unit encodes mature subunits of 18S, 5.8S and 28S rRNA. The
 CC ITS region lies between the 18S and 28S rRNA genes and contains two
 CC variable non-coding spacers (ITS1 and ITS2) and the 5.8S rRNA gene.
 XX
 SO Sequence 556 BP; 111 A; 168 C; 155 G; 122 T; 0 other;

Query Match 70.1%; Score 256; DB 20; Length 556;
 Best Local Similarity 88.5%; Pred. No. 5,8e-67;
 Matches 324; Conservative 0; Mismatches 35; Indels 7; Gaps 4;

QY 1 aaacttcaacaatgatactcttggctccgcatcgatgaagaacgacgaactgcgat 60
 |||||
 Db 175 aaacttcaacaacgatactcttggctccgcatcgatgaagaacgacgaactgcgat 234
 |||||
 QY 61 aagtaatgtaattgtaagattcaatgaatcagatcgtttgaacgacattgcgccc 120
 |||||
 Db 235 aagtaatgtaattgtaac-aatcagtgaaatcagatcgtttgaacgacattgcgccc 293
 |||||
 QY 121 ctggcatccgaggagcgtcgtcgcagcgatcgtcgtccctcaagcccgcttgc 180
 |||||
 Db 294 ctggatccgaggagcgtcgtcgcagcgatcgtcgtccctcaagcccgcttgc 353
 |||||
 QY 181 tcttggtcgtcgtcccccgcgggggagcgcccgaaagcgagcgcgacgcg-gt 239
 |||||
 Db 354 tcttggtcgtcgtcccccgcgggggagcgcccgaaagcgagcgcgacgcg-gt 413
 |||||
 QY 240 cgggtcctcagcgatgagtggtggtccgcatcgatgaaggcgagcgcgacgcg 299
 |||||
 Db 414 cgggtcctcagcgatgagtggtggtccgcatcgatgaaggcgagcgcgacgcg 471
 |||||
 QY 300 cgggcgtcccaacatcattcttcaggttgaccccgatcagtgatgaataccgcgtga 359
 |||||
 Db 472 cgatcaaccacaattt---tatacaggtgaccccgatcagtgatgaataccgcgtga 528
 |||||
 QY 360 acttaa 365
 |||||
 Db 529 acttaa 534

RESULT 5
 AAV70848
 ID AAV70848 standard; DNA: 355 BP.
 XX
 AC AAV70848;
 XX
 DT 26-FEB-1999 (first entry)
 XX
 DE Sequence containing the rDNA internal transcribed spacer 2 (ITS2).
 XX

KW 5.8S ribosomal RNA gene; internal transcribed spacer 2; ITS2;
 KW 28S ribosomal RNA gene; probe: Aspergillus flavus; A. fumigatus;
 KW A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
 KW Mucor rouxii; M. racemosus; M. plumbeus; M. indicus;
 KW M. circinniloides f. circinneloides; Rhizopus oryzae; R. microsporus;
 KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
 KW Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
 KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
 KW
 XX

OS Aspergillus terreus.

PN WO9850584-A2.

PD 12-NOV-1998.

PF 01-MAY-1998; 98WO-US08926.

PR 02-MAY-1997; 97US-0045400.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Aldorevich L, Choi JS, Morrison CJ, Relas E;

PI
 XX

DR WPI; 1999-034737/03.
 XX
 PT New nucleic acid probes for filamentous fungi - for detecting e.g.
 PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
 PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
 PT species.
 XX

PS Claim 1; Page 11; 45pp; English.

CC The present sequence represents a partial 5.8S ribosomal RNA gene,
 CC internal transcribed spacer 2 (ITS2), and a partial 28S ribosomal RNA
 CC gene. Probes can be derived from the present sequence which are
 CC species-specific. The specification also describes ITS2 sequence-derived
 CC probes for identifying a species selected from Aspergillus flavus,
 CC A. fumigatus, A. niger, A. terreus, A. nidulans, Fusarium solani,
 CC F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus, M. indicus,
 CC M. circinniloides f. circinneloides, Rhizopus oryzae, R. microsporus,
 CC R. circinans, R. stolonifer, Rhizomucor pusillus, Absidia corymbifera,
 CC Cunninghamella elegans, Pseudallesheria boydii (teleomorph of
 CC Scedosporium apiospermum), Penicillium notatum, or Sporothrix schenckii.
 CC The probes can be used for differentiating filamentous fungal species
 CC from each other and from other medically important fungi.
 XX

SQ Sequence 355 BP; 62 A; 105 C; 103 G; 85 T; 0 other;

Query Match 63.1%; Score 230.4; DB 20; Length 355;
 Best Local Similarity 87.6%; Pred. No. 2.3e-59;
 Matches 312; Conservative 0; Mismatches 31; Indels 13; Gaps 5;

QY 1 aaacttcaacaatgatactcttggctccgcatcgatgaagaacgacgaactgcgat 60
 |||||
 Db 1 aaacttcaacaatgatactcttggctccgcatcgatgaagaacgacgaactgcgat 60
 |||||
 QY 61 aagtaatgtaattgtaagattcaatgaatcagatcgtttgaacgacattgcgccc 120
 |||||
 Db 61 aagtaatgtaattgtaagattcaatgaatcagatcgtttgaacgacattgcgccc 120
 |||||
 QY 121 ctggcatccgaggagcgtcgtcgcagcgatcgtcgtccctcaagcccgcttgc 179
 |||||
 Db 121 ctggatccgaggagcgtcgtcgcagcgatcgtcgtccctcaagcccgcttgc 180
 |||||
 QY 180 ggttggtcgtcgtcccccgcgggggagcgcccgaaagcgagcgcgacgcg 237
 |||||
 Db 181 ggttggtcgtcgtcccccgcgggggagcgcccgaaagcgagcgcgacgcg 240
 |||||
 QY 238 -gtcgggtcctcagagcgatgagtggttgtaaccgcgtcgaataaggcgccggcgcc 296
 |||||
 Db 241 cgtcgggtcctcagagcgatgagtggttgtaaccgcgtcgaataaggcgccggcgcc 299
 |||||

RESULT 6
 AAA72782
 ID AAA72782 standard; DNA: 382 BP.
 XX

AC AAA72782;

DT 13-DEC-2000 (first entry)

DE 5.8S rRNA gene sequence.

XX Black spot disease; brown spot disease; fungi; fruit vegetable;
 KW field crop; Alternaria; 5.8S rRNA; detection; ds.
 XX

OS Aspergillus flavus.

PN WO200046397-A1.

PD 10-AUG-2000.

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XX 24-JAN-2000: 2000WO-US01466.
PF XX
XX 02-FEB-1999: 990US-0241427.
PR XX
XX (TECR ) TECHNION RES & DEV FOUND LTD.
PA (KASH/) KASHI Y.
XX PI
XX Kashi Y, Zur G, Sharf R, Hallerman E;
XX DR
XX WPI: 2000-499381/44.
XX
XX Nucleic acid based assay and kit for detection of Alternaria
PT contamination in food products involves analysing the sample of food
PT product for nucleic acid sequences unique to Alternaria
XX
XX Examples: Fig 1: 47pp; English.
XX
XX The invention relates to a nucleic acid based method for the detection
CC of Alternaria contamination in a food product. The method involves
CC obtaining and analysing a food product sample for a nucleic acid sequence
CC unique to Alternaria. Detectable levels of the nucleic acid sequence can
CC be used as an indication of Alternaria contamination. Fungi from the
CC genus Alternaria are ubiquitous saprophytes and are economically
CC important pathogens affecting a wide range of plants. Alternaria are the
CC causative agents of black or brown spot disease in many fruits,
CC vegetables and field crops. The method is used for the detection of
CC Alternaria contamination in food products. The present sequence
CC represents the Aspergillus flavus 5.8S rRNA gene, used in examples
CC illustrating the invention.
XX
XX Sequence 382 BP: 72 A; 111 C; 114 G; 84 T; 1 other:
SO
Query Match 60.6%; Score 221.2; DB 21; Length 382;
Best Local Similarity 94.2%; Pred. No. 1.4e-56;
Matches 262; Conservative 0; Mismatches 13; Indels 3; Gaps 3;
QY 1 aaacttcaacaatgagatcctctgttcgagcatcgatgaagaagcagcgactgcgat 60
DB 98 aaacttcaacaatgagatcctctgttcgagcatcgatgaagaagcagcgactgcgat 157
QY 61 aagtaatgtgaattgcagaatcagatcagatcagatcgtttgaagcagcatgcgcc 120
DB 158 aactatgtgaattgcagaatcagatcagatcagatcgtttgaagcagcatgcgcc 217
QY 121 ctggacttcgggggagcatcgttcgagcgatcgttcgttcgc-cgaagccggctgtg 179
DB 218 ctggatctccgggggagcatcgttcgagcgatcgttcgttcgc-cgaagcagcgctgtg 277
QY 180 gtgttggtcgttcgttcgcc-cgccccggggagcagcgccgaaagcagcgccagcg- 237
DB 278 gtgttggtcgttcgttcgccccctcccgggggagcagcgcccaagagcagcgccagcg 337
QY 238 gtccggtcctcgagcgatcgagggctgttcacccgctc 275
DB 338 gtccggtcctcgagcgatcgagggctgttcacccgctc 375
RESULT 7
AA222437
ID AA222437 standard; DNA: 498 BP.
XX
XX AA222437:
XX
XX 02-DEC-1999 (first entry)
XX
XX Internal Transcribed Spacer of P.crustosum.
XX
XX Internal Transcribed Spacer; ITS: fungus; yeast; fermentation; assay;
KM PCR; microorganism; wine-making; commercial; ds.
XX
XX Penicillium crustosum.
OS

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XX XX
XX PN WO9946405-A1.
XX XX
XX PD 16-SEP-1999.
XX XX
XX PF 11-MAR-1999; 99WO-US04251.
XX XX
XX PR 11-MAR-1998; 98US-0037990.
XX XX
XX PA (GALL-) GALLO WINERY E & J.
XX PI
XX Engel SR, Descenzo RA, Morenzoni RA, Irelan NA;
XX DR
XX WPI: 1999-551425/46.
XX
XX New isolated fungal and yeast nucleic acids, used for identifying
PT different fermentation-related microorganisms, particularly in wine
PT fermentation cultures
XX
XX Disclosure: Page 32; 52pp; English.
XX
XX This is the nucleotide sequence for the Internal Transcribed Spacer
CC (ITS) of P.crustosum. This sequence was amplified directly from the
CC isolate by the ITS5 (AA222530) and ITS4 (22531) primers.
CC This invention is directed to the identification of different
CC fermentation related microorganisms, particularly those involved in the
CC production of wine. The invention utilizes a polymerase chain reaction
CC (PCR) based diagnostic assay of DNA sequences located in the Internal
CC Transcribed Spacer (ITS) region of the ribosomal RNA gene.
CC Ribosomal genes are suitable for use as molecular probe targets because
CC of their high copy number. Non transcribed and transcribed spacer
CC sequences associated with ribosomal genes are usually poorly conserved
CC and, thus, are advantageously used as target sequences for the detection
CC of recent evolutionary divergence. Fungal rRNA genes are organized in
CC units. Each unit encodes mature subunits of 18S, 5.8S and 28S rRNA. The
CC ITS region lies between the 18S and 28S rRNA genes and contains two
XX variable non-coding spacers (ITS1 and ITS2) and the 5.8S rRNA gene.
XX
XX Sequence 498 BP: 93 A; 154 C; 139 G; 112 T; 0 other:
SO
Query Match 60.4%; Score 220.6; DB 20; Length 498;
Best Local Similarity 90.8%; Pred. No. 2.3e-56;
Matches 268; Conservative 0; Mismatches 24; Indels 3; Gaps 3;
QY 1 aaacttcaacaatgagatcctctgttcgagcatcgatgaagaagcagcgactgcgat 60
DB 176 aaacttcaacaatgagatcctctgttcgagcatcgatgaagaagcagcgactgcgat 235
QY 61 aagtaatgtgaattgcagaatcagatcagatcagatcgtttgaagcagcatgcgcc 120
DB 236 agtaatgtgaattgcagaatcagatcagatcagatcgtttgaagcagcatgcgcc 294
QY 121 ctggacttcgggggagcatcgttcgagcgatcgttcgttcgc-cgaagccggctgtg 180
DB 295 ctggatctccgggggagcatcgttcgagcgatcgttcgttcgc-cgaagcagcgctgtg 354
QY 181 gtgttggtcgttcgttcgcc-cgccccggggagcagcgccgaaagcagcgccagcg-g 238
DB 355 gtgttggtcgttcgttcgccccctcccgggggagcagcgccgaaagcagcgccagcg 414
QY 239 tcgggtcctcgagcgatcgagggctgttcacccgctcgatgaagcgccggcg 293
DB 415 tcgggtcctcgagcgatcgagggctgttcacccgctcgatgaagcgccggcgcg 469
RESULT 8
AA290111
ID AA290111 standard; DNA: 610 BP.
XX
XX AA290111:
XX
XX 17-SEP-1999 (first entry)
XX

```


Db 60 ttgcgcccccttgatttccgggggagatgctctgltccgagcgtcatgtctgcacctcaagca 119

Oy 172 cggctctgtctgttgcgtgcgtctcccccgggggagccgggagccgaaagcagcgcg 231
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 120 cggctctgtctgttgcgtgcgtctcccccgggggagccgggagccgaaagcagcgcg 179

Oy 232 gacccg-gtccggtccctcagcgtatggggtctgtgtacccgctcgatataggcgcgcg 290
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 180 gacccgctcgcgtctcctcagcgtatggggtctgtgtacccgctc--tgtaggccggcgcc 237

Oy 291 ggcgcgacgcggcgctcccaacctatcttctcaagcttgacctcgatcgatcagttaaggat 350
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 238 ggcgtctgcgataccaaccaattt---ttaccaggttgacctcgatcagttaaggat 294

Oy 351 acccgctgaactta 365
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 295 acccgctgaactta 309

RESULT 10
AAx90112
ID AAx90112 standard; DNA; 568 BP.
XX
XX
AC AAx90112;
XX
DT 17-SEP-1999 (first entry)
XX
XX
DE Diplodia gossypina Internal transcribed spacer DNA sequence.
XX
XX ITS1; ITS2; Internal transcribed spacer; detection; fungal pathogen;
KM grape; ribosomal RNA gene region; identification; wine; ds.
XX
XX
OS Diplodia gossypina.
XX
PN WO9229899-A1.
XX
PN 17-JUN-1999.
XX
XX 07-DEC-1998; 98WO-US25210.
XX
XX 08-DEC-1997; 97US-0986727.
XX
XX (GALL-) GALLO WINERY E & J.
XX
XX
PI Descenzo RA, Engel SR, Ireland NA;
XX
XX WPI; 1999-429921/36.
XX
XX
PT Novel primers targeted to Internal transcribed spacer region of
XX fungal pathogen ribosomal DNA genes
XX
XX
PS Disclosure; Page 32-33; 43pp; English.
XX
XX
XX The present invention describes oligonucleotides (I) for identifying
CC fungal pathogens, especially of grape plants. The oligonucleotides
CC are isolated double stranded nucleic acids representing the internal
CC transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the
CC organisms *Eutypella vitis*, *Eutypa lata*, *Phomopsis viticola* or
CC *Diplodia gossypina*. The oligonucleotides are used to detect the fungal
CC pathogen *Eutypella vitis*, *Eutypa lata*, *Phomopsis viticola* or *Diplodia*
CC *gossypina*, especially when infecting grape plants. The detection method
CC is used in the wine industry. AAx90075 to AAx90094 represent
CC specifically claimed oligonucleotides from the present invention.
CC AAx90095 to AAx90105 represent specifically claimed PCR primers for use
CC in the detection of the fungal pathogens *Eutypella vitis*, *Eutypa lata*,
CC *Phomopsis viticola* or *Diplodia gossypina*. The present sequence represents
CC an ITS DNA sequence from the present invention.
XX
XX
XX Sequence 568 BP; 142 A; 147 C; 144 G; 135 T; 0 other;

Query Match	55.8%;	Score 203.8;	DB 20;	Length 568;
Best Local Similarity	76.4%;	Pred. No. 2.5e-51;		

Matches	279; Conservative	0; Mismatches	77; Indels	9; Gaps	2
QY	1 aaacttcaacaatgactctcttggltccgcgacatcgtaaagcagcgaaactcgat	60			
Db	191 aaacttcaacaacagactctcttggltccgcgacatcgtaaagcagcgaaactcgat	250			
QY	61 aagtaaatgtaattgcctgattcagtgatatacgaagcttttgaaacgacattggcgccc	120			
Db	251 aagtaaatgtaattgcctgattcagtgatatacgaagcttttgaaacgacattggcgccc	310			
QY	121 ctggcattccgggggcacatgcctgtccgcagcgatcatcttccctcaacgcgagctgtg	180			
Db	311 ctggatctccgggggcacatgcctgtgttcgagcgcatctatcaacccctcaagcttgcgtg	368			
QY	181 tcttgggtgcgtgcccccgcgggggaacggccgaagcagcgcgcgcaacggcgtc	240			
Db	369 ----gaatttggacacgctctcactctgcggacgcgctcgaagacctcggcggtgtcgtt	424			
QY	241 cgtgcctcagcgctaaagggcgttggttcacacgcgctcgtattaaaggccggcgccgcagcc	300			
Db	425 cagcgcctccaagcgttagtaagaatacaacctgcgtcttggatgtgttggtgcgtccgcgcgac	484			
QY	301 ggcgtctccaaccttacttctcaggttgtaacctcgcgatcagtgtaaggataccgcgtgaa	360			
Db	485 gaacctctcgaacttctct----caaggttgacctcgtgcgatcagtgtaaggataccgcgtgaa	541			
QY	361 cttaa 365				
Db	542 cttaa 546				

Accession	Species	Gene	Region	Seq ID	Length (bp)	GC Content (%)	Notes
AAH73767	standard	DNA	640	BP			
AAH73767							
08-OCT-2001		(first entry)					
Guignardia citricarpa	RNA gene	ITS region	SEQ ID NO:4				
Ribosomal RNA gene	RNA gene	Internal transcribed spacer	ITS				
pachosensis	citrus blackspot disease	citrus fruit	differentiation				
characterisation	detection	ds					
Guignardia citricarpa							
Key	Location/Qualifiers						
1..32	/*tag- a	/partial	/product= "18S ribosomal RNA"				
33..266	/*tag- b	/note= "Internal transcribed spacer (ITS) 1"					
267..424	/*tag- c	/product= "5.8S ribosomal RNA"					
425..589	/*tag- d	/note= "Internal transcribed spacer (ITS) 2"					
590..640	/*tag- e	/partial	/product= "28S ribosomal RNA"				
26-JUL-2001							
19-JAN-2001							
2001MO-US01735							
2000US-0177013							

```
XX PA (UWOR-) UNIV OREGON.
XX PI Carroll GC:
XX DR WPI: 2001-465362/50.
XX PT New differentiating oligonucleotides which hybridizes with a target DNA
XX PT sequence associated with pathogenic or non-pathogenic species of
XX PT Guignardia, for differentiating pathogenic from non-pathogenic species
XX PT
XX PS Claim 11: Fig 1: 33pp: English.
XX CC The invention relates to oligonucleotide amplification primers and
XX CC methods for the detection of pathogenic Guignardia citricarpa. Guignardia
XX CC citricarpa is a fungus which causes citrus blackspot disease, producing
XX CC progressive black surface lesions on the fruits of most commercial citrus
XX CC cultivars such as oranges, lemons, limes, and grapefruit. Although this
XX CC is a cosmetic disease, it causes significant losses to the citrus fruit
XX CC growing industry, as many countries do not permit the importation of
XX CC affected fruit. However, there is a second, non-pathogenic Guignardia
XX CC species, Guignardia citricarpa, which also infects citrus fruit, but
XX CC which forms insignificant lesions. This non-pathogenic Guignardia species
XX CC is morphologically almost indistinguishable from the pathogenic
XX CC Guignardia citricarpa, and both species may be simultaneously present on
XX CC one fruit. The primers of the invention are targeted to the internal
XX CC transcribed spacer (ITS) regions of the ribosomal RNA gene of either the
XX CC pathogenic Guignardia citricarpa (see AAH73768) or the non-pathogenic
XX CC Guignardia citricarpa (see AAH73768). These regions exhibit significant
XX CC differences between the two species, and provides a means by which the
XX CC two species may be distinguished from one another. The present sequence
XX CC represents the rRNA gene ITS region of the pathogenic Guignardia
XX CC citricarpa.
XX SO Sequence 640 BP; 152 A; 167 C; 169 G; 152 T; 0 other:

Query Match 53.5%; Score 195.2; DB 22; Length 640;
Best Local Similarity 74.7%; Pred. No. 1e-48;
Matches 275; Conservative 0; Mismatches 83; Indels 10; Gaps 2;

OY 1 aaacttcaacatgagctcttggttcggcatgcatgaaagaacgagcaatcgcat 60
DB 267 aaacttcaacacgagatctcttggttcggcatgaaagaacgagcaatcgcat 326
OY 61 aagtaatgtaactgcaagaatcaatgaatcatcgagctcttgaacgacatcgcc 120
DB 327 aagtaatgtaactgcaagaatcaatgaatcatcgagctcttgaacgacatcgcc 386
OY 121 ctggcattccgggggagcatgctctgctcgagcgatcatgctccctcaagccggcttg 180
DB 387 ctggcattccgggggagcatgctctgctcgagcgatcatgctccctcaagccggcttg 446
OY 181 tgttggtcgtctgctcccccgggggagcgagccgaaagcgagcgagccgctc 240
DB 447 attgg-----gagcagctccgctcgcgagcgagcctcgagcgagcgctc 499
OY 241 cggctccgagcgataggggcttggttcaacccgctcgatagggccgggagcgccaccc 300
DB 500 cggctccgagcgataggttaataatctcgcgttggaaggaaggggcgctgagcgagc 559
OY 301 ---ggcgtcccaacctatctctcaggtgagcctcgatcaggtaggaataccgct 357
DB 560 aatcgacctcgctacatatttccaaaggtgacctcgatcaggtaggaataccgct 619
OY 358 gaacttaa 365
DB 620 gaacttaa 627
```

RESULT 12
AAK90110

```
ID AAK90110 standard; DNA; 608 BP.
XX AC AAK90110;
XX DT 17-SEP-1999 (first entry)
XX DE Phomopsis viticola (variant 1) Internal transcribed spacer DNA sequence.
XX KM ITS1; ITS2: Internal transcribed spacer; detection: fungal pathogen;
XX KM grape; ribosomal RNA gene region; Identification: wine; ds.
XX OS Phomopsis viticola.
XX PN WO929899-A1.
XX PD 17-JUN-1999.
XX PF 07-DEC-1998; 98WO-US25210.
XX PR 08-DEC-1997; 97US-0986727.
XX PA (GALL-) GALLO WINERY E & J.
XX PI Descenzo RA, Engel SR, Ireland NA.
XX DR WPI: 1999-429921/36.
XX PT Novel primers targeted to internal transcribed spacer region of
XX PT fungal pathogen ribosomal DNA genes
XX PS Disclosure; Page 31; 43pp: English.
XX CC The present invention describes oligonucleotides (I) for identifying
XX CC fungal pathogens, especially of grape plants. The oligonucleotides
XX CC are isolated double stranded nucleic acids representing the internal
XX CC transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the
XX CC organisms Eutypella vitis, Eutypa lata, Phomopsis viticola or
XX CC Diplodia gossypina. The oligonucleotide are used to detect the fungal
XX CC pathogens Eutypella vitis, Eutypa lata, Phomopsis viticola or Diplodia
XX CC gossypina, especially when infecting grape plants. The detection method
XX CC is used in the wine industry. AAX90075 to AAX90094 represent
XX CC specifically claimed oligonucleotides from the present invention.
XX CC AAX90095 to AAX90105 represent specifically claimed PCR primers for use
XX CC in the detection of the fungal pathogens Eutypella vitis, Eutypa lata,
XX CC Phomopsis viticola or Diplodia gossypina. The present sequence represents
XX CC an ITS DNA sequence from the present invention.
XX SO Sequence 608 BP; 154 A; 166 C; 153 G; 135 T; 0 other:

Query Match 51.6%; Score 188.4; DB 20; Length 608;
Best Local Similarity 75.4%; Pred. No. 1.e-46;
Matches 276; Conservative 0; Mismatches 81; Indels 9; Gaps 3;

OY 1 aaacttcaacatgagctctcttggttcggcatgcatgaaagaacgagcaatcgcat 60
DB 231 aaacttcaacacgagatctcttggttcggcatgcatgaaagaacgagcaatcgcat 290
OY 61 aagtaatgtaactgcaagaatcaatgaatcatcgagctcttgaacgacatcgcc 120
DB 291 aagtaatgtaactgcaagaatcaatgaatcatcgagctcttgaacgacatcgcc 350
OY 121 ctggcattccgggggagcatgctctgctcgagcgatcatgctccctcaagccggcttg 180
DB 351 ctggatattccggaggagcatgctctgagcgatcatcttcaacccctcaagccttgctg- 409
OY 181 tgttggtcgtctgctcccccgggggagcgagccgaaagcgagcgagccgctc 240
DB 410 tgaatgggacctctcttaccaggaagagcagcgccgaatcaatgagcgagctg--- 466
OY 241 cggctccgagcgataggggcttggttcaacccgctcgatagggccgggagcgccaccc 300
DB 467 -----ccagagcccgagcgagcatagtaaacctcgtctctggaagcgcttgagctgcc 522
```


Oy	301	ggcgctcccaacctatctt- tctcaggttgaacctggaatgaaggaataccgcgtga	359
Db	523	tgcgctaaccaccaactctctgaaaattgacctggaatcaggtcaggaataaccgcctga	582
Oy	360	actaa	365
Db	583	actaa	588
RESULT 13			
ID	AAH73768	AAH73768 standard; DNA; 618 BP.	
AC	AAH73768;		
DT	08-OCT-2001	(first entry)	
XX			
DE	Guignardia citricarpa1	rRNA gene ITS region, seq ID NO:5.	
XX			
KM	Ribosomal RNA gene; rRNA gene; internal transcribed spacer; ITS;		
KW	non-pathogenic; citrus blackspot disease; citrus fruit; differentiation;		
XX	characterisation; detection; ds.		
OS	Guignardia citricarpa.		
XX			
PH	Key	Location/Qualifiers	
FT	rRNA	1..31	
FT		/*tag= a	
FT		/partial	
FT	misc_feature	/product= "18S ribosomal RNA"	
FT		32..261	
FT		/*tag= b	
FT	rRNA	/note= "Internal transcribed spacer (ITS) 1"	
FT		262..419	
FT		/*tag= c	
FT	misc_feature	/product= "5.8S ribosomal RNA"	
FT		420..582	
FT		/*tag= d	
FT	rRNA	/note= "Internal transcribed spacer (ITS) 2"	
FT		583..618	
FT		/*tag= e	
FT		/partial	
XX		/product= "28S ribosomal RNA"	
PN	WO200153318-A2.		
XX			
PD	26-JUL-2001.		
XX			
PF	19-JAN-2001; 2001WO-US01735.		
XX			
PR	19-JAN-2000; 2000US-0177013.		
XX			
PA	(UYOR-) UNIV OREGON.		
XX			
PI	Carroll GC;		
XX			
DR	WPI: 2001-465362/50.		
XX			
XX			
PT	New differentiating oligonucleotides which hybridizes with a target DNA		
PT	sequence associated with pathogenic or non-pathogenic species of		
PT	Guignardia, for differentiating pathogenic from non-pathogenic species		
PT	-		
XX			
PS	Claim 14; Fig 2; 33pp; English.		
XX			
CC	The invention relates to oligonucleotide amplification primers and		
CC	methods for the detection of pathogenic Guignardia citricarpa. Guignardia		
CC	citricarpa is a fungus which causes citrus blackspot disease, producing		
CC	progressive black surface lesions on the fruits of most commercial citrus		
CC	cultivars such as oranges, lemons, limes, and grapefruit. Although this		
CC	is a cosmetic disease, it causes significant losses to the citrus fruit		
CC	growing industry, as many countries do not permit the importation of		

CC	affected fruit. However, there is a second, non-pathogenic <i>Gulgnardia</i>
CC	species, <i>Gulgnardia citlicarpa</i> , which also infects citrus fruit, but
CC	which forms insignificant lesions. This non-pathogenic <i>Gulgnardia</i> species
CC	is morphologically almost indistinguishable from the pathogenic
CC	<i>Gulgnardia citlicarpa</i> , and both species may be simultaneously present on
CC	one fruit. The primers of the invention are targeted to the internal
CC	transcribed spacer (ITS) regions of the ribosomal RNA gene of either the
CC	pathogenic <i>Gulgnardia citlicarpa</i> (see AAH73767) or the non-pathogenic
CC	<i>Gulgnardia citlicarpa</i> (see AAH73768). These regions exhibit significant
CC	differences between the two species, and provides a means by which the
CC	two species may be distinguished from one other. The present sequence
CC	represents the rRNA gene ITS region of the non-pathogenic <i>Gulgnardia</i>
CC	<i>citlicarpa</i> .
SQ	Sequence 618 BP; 146 A; 159 C; 155 G; 158 T; 0 other;
XX	
Query Match	50.4%; Score 184; DB 22; Length 618;
Best Local Similarity	73.1%; Pred. No. 2,2e-45;
Matches 265; Conservative	0; Mismatches 90; Indels 8; Gaps 2
OY	1 aaacttcaacaatgagatctcttggtccggacatgaagaacgcagcgaactcgat 60
DB	262 aaactttcaacaacgagatctcttggtccggacatgaagaacgcagcgaatcgat 321
OY	61 aagtaattgaaattggaagaattcagtgaaatcatcgatctcttgaacgcacattgcgcc 120
DB	322 aagtaattggaattggaagaattcagtgaaatcatcgatctcttgaacgcacattgcgcc 381
OY	121 ctggacctccggagggcagtgcctgttcgaacggtcattgctgcctcaaacccggcttgt 180
DB	382 ctgtaattccggagggcagtgcctgttcgaacggtcatttcaaccctcaaatctctgtgt 441
OY	181 tgttggtctgtctgtcccccccgggggaagccggccaagcagcggcggaaccggc 240
DB	442 attgg-----gcaacgtccgctccgggaacgtgcttgaagaacctcggcgacggc 494
OY	241 cgttcctcagagcgtatgggggctgtgacccgctcgaattagagccggccggcgccag-c 299
DB	495 tagcctcagagcgtatggaaataatctcgtcttgtagtgctggggaggaagccgcggac 554
OY	300 cggcgctccaacctatctcttcacaggttacctcgatcgatcagtagtataccgcgtga 359
DB	555 aatcgacctcgtctatcttttccaaggttgacctcgatatcagtagtataccgcgtga 614
OY	360 acct 363
DB	615 acct 618
RESULT 14	
AAV43265	
ID	AAV43265 standard; DNA; 597 BP.
XX	
AC	AAV43265;
XX	
DT	26-OCT-1998 (first entry)
XX	
DE	Sequence of ITS region from <i>Kabatella zeeae</i> , isolate 56351.
XX	
KW	Internal transcribed spacer; ITS; detection; maize; fungal pathogen; ss.
OS	
XX	<i>Kabatella zeeae</i> .
XX	
PH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	1..30
FT	/tag= a
FT	/note= "3' end of small subunit rRNA gene"
FT	31..217
FT	/tag= b
FT	/note= "ITS1"
FT	218..373
FT	/tag= c
FT	misc_feature
FT	C

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FT      misc_feature      /note="5.8S rRNA gene"
FT      374..540
FT      /tag= d
FT      /note= "ITS2"
FT      misc_feature      /tag= e
FT      541..597
FT      /note= "5' end of large subunit rRNA gene"
XX
XX      EP859061-A2.
XX
XX      19-AUG-1998.
XX
XX      03-NOV-1997.      97EP-0810779.
XX
XX      01-NOV-1996.      96US-0742023.
XX
XX      (NOVS ) NOVARTIS AG.
XX
XX      Beck JJ:
XX
XX      WPI: 1998-429687/37.
XX
XX      New internal transcribed spacer sequences of maize fungal pathogens
XX      PT and primers and primer pairs - used to detect pathogens e.g.
XX      PT Helminthosporium carbonum, Cercospora zeae-maydis and Kabatiella
XX      PT zeae
XX
XX      Claim 2: Pages 19-20; 49pp; English.
XX
XX      AAV42363-70 represent internal transcribed spacer (ITS) DNA sequences
XX      CC that are unique to the organisms from which they are isolated. The
XX      CC specification describes a method for the detection of a maize fungal
XX      CC pathogen. The method comprises isolating DNA from a plant leaf
XX      CC infected with a pathogen, subjecting the DNA to PCR amplification
XX      CC using at least one primer derived from the ITS sequence (see
XX      CC AAV43277-303).
XX
XX      Sequence 597 BP; 146 A; 156 C; 153 G; 142 T; 0 other:

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Query Match      49.5%; Score 180.6; DB 19; Length 597;
Best Local Similarity 72.2%; Pred. No. 2.3e-44;
Matches 265; Conservative 0; Mismatches 94; Indels 8; Gaps 2;

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OY      1 aaacttcaacaatgatactcttggttcgcgcatcgatgaagaacgagcaactcgat 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      217 aaacttcaacaacgatactcttggttcgcgcatcgatgaagaacgagcaactcgat 276
OY      61 aagtaatgtaattcagaattcagtaatcagatcgaatttgaacgacattgcgcc 120
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      277 aagtaatgtaattcagaattcagtaatcagatcgaatttgaacgacattgcgcc 336
OY      121 ctggcattccggggcgatcctctcgtccagcgatcgtccctcaagccgagctgtg 180
      ||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      337 ctggatctcgaaggcgatcctctcgtccagcgatcgtccctcaagctcgtctg-- 394
OY      181 tgttggtcgtcgtcccccgcggggagcgagccgaaagcgagcgagcagcgatc 240
      || || || || || || || || || || || || || || || || || || || || ||
DB      395 ----glatggcgctcgtcctctcggggcgagcgcccaaacctcggagagccctcac 450
OY      241 cgggccctcgagcgatggggtcgtgtacccgctcgaattagggcgccggggcgccagcc 300
      ||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      451 cgggttcagcgctagtgaaattcattcaatcaacgactcgtgcgaaacccgaggggaaattct 510
OY      301 ggcgtctccaaac--tatactcttcagatgtgacctcgatcagatcagatagatcccgctg 358
      || | | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
DB      511 ggcgaagaagaaccttataattcttagtgatgacctcgatcagatcagatagatagatcccgctg 570
OY      359 aacttaa 365
      |||||
DB      571 aacttaa 577

```

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RESULT 15
AAV59009
ID      AAV59009 standard; DNA; 561 BP.
XX
XX      AAV59009;
XX
XX      06-JAN-1999 (first entry)
XX
XX      F. avenaceum Internal transcribed spacer.
XX
XX      Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
XX      KM fungal pathogen identification; infection identification; ss.
XX
XX      Fusarium avenaceum.
XX
XX      Key Location/Qualifiers
XX      FH misc_feature 31..181
XX      FT /tag= a
XX      FT /note= "ITS1"
XX      FT misc_feature 339..504
XX      FT /tag= b
XX      FT /note= "ITS2"
XX
XX      US5827695-A.
XX      PD 27-OCT-1998.
XX
XX      01-AUG-1997; 97US-0905314.
XX
XX      01-AUG-1997; 97US-0905314.
XX
XX      (NOVS ) NOVARTIS FINANCE CORP.
XX
XX      Beck JJ:
XX
XX      WPI: 1998-593995/50.
XX
XX      Wheat pathogen internal transcribed spacer sequences - used as a
XX      PT basis for primers for the species-specific polymerase chain reaction
XX      PT detection of the pathogens
XX
XX      Claim 1; Column 29-30; 20pp; English.
XX
XX      This sequence represents an internal transcribed spacer (ITS) sequence of
XX      CC the invention. The primer pairs, based on the ITS sequences, are used for
XX      CC the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX      CC pathogens, especially F. nivale, F. graminearum, F. culmorum,
XX      CC F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX      CC strains of fungi show different symptoms during infection, which may or
XX      CC may not be due to infection. Early identification of the strain causing
XX      CC the infection allows early, and more specific fungicidal treatment.
XX
XX      Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 3 other:

```

```

Query Match      49.4%; Score 180.2; DB 19; Length 561;
Best Local Similarity 71.8%; Pred. No. 3e-44;
Matches 265; Conservative 2; Mismatches 90; Indels 12; Gaps 2;

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```

OY      1 aaacttcaacaatgatactcttggttcgcgcatcgatgaagaacgagcaactcgat 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      181 aaacttcaacaacgatactcttggttcgcgcatcgatgaagaacgagcaactcgat 240
OY      61 aagtaatgtaattcagaattcagtaatcagatcgaatttgaacgacattgcgcc 120
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      241 aagtaatgtaattcagaattcagtaatcagatcgaatttgaacgacattgcgccg 300
OY      121 ctggcattccggggcgatcctctcgtccagcgatcgtccctcaagcc-----gact 176
      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      301 ctggatctcggggcgatcgtcgtgtacattcaacccctcaagcccgaggttc 360
OY      177 tgttggtcgtcgtcccccgcggggagcgagccgaaagcgagcgagcgacc 236
      |||| | ||| | || | | || | | || | | || | | || | | || | | || | | || | |

```

```

Db 361 ggtcttgaggatcgctctgctlmtygacgtgacgccccgaaatacattggcgtctc 420
Oy 237 ggtccggtctctgaggtatgaggcttggtacccgctcgattaggccggcgccgccc 296
Db 421 g-----ctgagcctccattgctgtagtaagctaaacctcgcaactggaacggcgcc 472
Oy 297 agccggcgtctccaacttattctctcaggttgacctcgatcaggtagggataccgc 356
Db 473 ggtcattgctgtaaaccccaactctctgaatgttgacctcgatcaggtaggaataccgc 532
Oy 357 tgaactta 365
Db 533 tgaactta 541

```

Search completed: August 21, 2002, 22:22:38
 Job time: 5778 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 18:03:41 ; Search time 5019.06 Seconds

(without alignments)
981.536 Million cell updates/sec

Title: US-10-046-955-5

Perfect score: 1 aaacttcaacatgatct.....gggatacccgctgaactaa 365

Sequence: IDENTITY_NUC

Scoring table: Gapop 10.0, Gapect 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	230	63.0	318	9	AI213025 Y6f01a1.f
C 2	188	51.5	213	9	AI209736 C7G08a1.f
3	178.8	49.0	227	9	AA965960 r8a05a1.r
4	149.2	40.9	189	9	AA783772 C7G08a1.r
5	143.8	39.4	882	12	CNS06XIS
6	142.2	39.0	1117	12	CNS07ARF
C 7	141.4	38.7	718	12	CNS06FTN
C 8	141.4	38.7	827	12	CNS06FMV
C 9	141.4	38.7	866	12	CNS06FV
C 10	141.4	38.7	869	12	CNS06DGL
C 11	141.4	38.7	889	12	CNS06DHL
12	141.4	38.7	902	12	CNS06CUX
13	141.4	38.7	928	12	CNS06F06
C 14	141.4	38.7	936	12	CNS06CB4
15	141.4	38.7	960	12	CNS06FXB
16	141.4	38.7	962	12	CNS06F02
C 17	141.4	38.7	1000	12	CNS06FNV

C 18	141.4	38.7	1006	12	CNS06CY	AL393152 T3 end of
C 19	141.4	38.7	1035	12	CNS06DA6	AL393556 T3 end of
C 20	141.4	38.7	1036	12	CNS06DOL	AL394147 T7 end of
21	141.4	38.7	1045	12	CNS06CNZ	AL392757 T3 end of
22	141.4	38.7	1048	12	CNS06CN3	AL392725 T3 end of
23	140	38.4	141	9	AI327879	AI327879 j0906a1.r
24	139.4	38.2	448	12	A2916873	A2916873 4911.f063
25	139.4	38.2	885	12	CNS06HJY	AL399092 T3 end of
C 26	139.4	38.2	922	12	CNS06HOU	AL399268 T7 end of
C 27	139.4	38.2	936	12	CNS06HIO	AL399046 T7 end of
28	139.4	38.2	943	12	CNS06I40	AL399814 T7 end of
C 29	139.4	38.2	950	12	CNS06JAK	AL401346 T3 end of
C 30	139.4	38.2	953	12	CNS06GAR	AL397429 T3 end of
C 31	139.4	38.2	961	12	CNS06HT1	AL399419 T3 end of
C 32	139.4	38.2	962	12	CNS06G9U	AL397432 T3 end of
C 33	139.4	38.2	963	12	CNS06J6C	AL401198 T7 end of
C 34	139.4	38.2	966	12	CNS06I1T	AL399735 T3 end of
C 35	139.4	38.2	977	12	CNS06J9K	AL401310 T3 end of
C 36	139.4	38.2	982	12	CNS06HM6	AL399172 T3 end of
C 37	139.4	38.2	985	12	CNS06JLS	AL401750 T3 end of
C 38	139.4	38.2	997	12	CNS06HOW	AL399342 T3 end of
C 39	139.4	38.2	1024	12	CNS06H7C	AL398638 T3 end of
C 40	139.4	38.2	1035	12	CNS06JNU	AL401813 T3 end of
C 41	139.2	38.1	214	10	BF251183	BF251183 EST418443
C 42	139	38.1	360	12	A2923094	A2923094 4908.g987
C 43	139	38.1	424	12	A2923253	A2923253 4908.gf20
C 44	139	38.1	456	12	A2923320	A2923320 4908.gf20
C 45	139	38.1	481	12	A0491983	A0491983 V11612 m

ALIGNMENTS

RESULT 1
AI213025/c
LOCUS
DEFINITION
Y6f01a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emricella nidulans cDNA clone y6f01a1 3', mRNA sequence.

ACCESSION
AI213025
VERSION
AI213025.1
KEYWORDS
EST.
SOURCE
Emricella nidulans.

ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emricella.

REFERENCE
1 (bases 1 to 318)
Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.

TITLE
An Aspergillus nidulans EST Database

JOURNAL
Unpublished (1998)

COMMENT
Other-ESTs: Y6f01a1.f1
Contact: Bruce A. Roe, University of Oklahoma, broeou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeou.edu

We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: M13-20
High quality sequence stop: 265.
Location/Qualifiers
1..318

FEATURES
source
/organism="Emricella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="y6f01a1"
/clone_1lb="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI: 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"

Query Match 63.0%; Score 230; DB 9; Length 318;
Best Local Similarity 98.4%; Pred. No. 1.3e-46;
Matches 254; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

OY 1 aaacttcaacaatgagatctctgtgtccgcatcgtatgaagaacgacgaaatcgat 60
|||
Db 255 AAATTTCAACAATGATCTCTGTCCGGCATGCATGAACAGCAGAACTCGAT 196
|||
OY 61 aagaaatgtaatttcgaattcaatgaattcagatcgtcttgaagacatctgcccc 120
|||
Db 195 AAGTAATGTAATTCAGAAATTCAGTAATCATGAGATCTTTGAACGACATTTGCCCCC 136
|||
OY 121 ctggcatccgggggacatgcctgcagagcgatcgtctgcctcaagccgactgtg 180
|||
Db 135 CTGGCATTCGGGGGGCATGCTCGAGCGATTCGTCGCCCTCAAGCCCGCTTGG 76
|||
OY 181 tgttggt 239
|||
Db 75 TGTGGGTCTGTCTGT---CCGCCCGGGGAGCGGCCGGAAGGACGCGCGCATCTGT 19
|||
OY 240 ccggtcctcagcgatg 257
|||
Db 18 CCGGTCTCTCAGCGCTATG 1
|||

RESULT 2
AI209736 213 bp mRNA linear EST 19-OCT-1998
LOCUS c7g08a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
DEFINITION
c7g08a1.3', mRNA sequence.
ACCESSION
AI209736
VERSION
AI209736.1 GI:3771678
KEYWORDS
EST.
SOURCE
Emericella nidulans.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
REFERENCE
1 (bases 1 to 213)
Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
Prade, R. and Roe, B.
An Aspergillus nidulans EST Database
unpublished (1998)
OTHER_FEATURES: c7g08a1.f1
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: M13-20.

FEATURES

source

Location/Qualifiers
1..213
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="c7g08a1"
/clone_1lb="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 43 a 68 c 63 g 39 t

ORIGIN

Query Match 51.5%; Score 188; DB 9; Length 213;
Best Local Similarity 98.1%; Pred. No. 2.5e-36;
Matches 212; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

OY 41 agaagcgaggaactgcgataagtaatgtaattcgaattcagatcagatcgt 100
|||
Db 213 AAGAACGACGCAATCGCATTAATGTGAATTCACAATTCAGTGAATCATCGAGCTT 154
|||
OY 101 ttgaacgacatttgccccctgcgtatccgggggacatgcctcgcagcgatcgt 160
|||
Db 153 TTGAACGACATTCGCGCCCTGGCATTCGGGGGACATGCTTCCAGCGCTATTGCT 94
|||
OY 161 gccctcaagcccggt 220
|||
Db 93 GCCCTCAAGCCCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 37
|||
OY 221 aggcagcgagcgacgg-gtccggtcctcagcgata 255
|||
Db 36 AGCGACGGCGGCGACCGTCTCGATCGAGCGTA 1
|||

RESULT 3
AA965960 227 bp mRNA linear EST 31-JUL-1998
LOCUS r8a05a1.f1 Aspergillus nidulans 24hr asexual developmental and
vegetative cDNA lambda zap library Emericella nidulans cDNA clone
DEFINITION
r8a05a1.5', mRNA sequence.
ACCESSION
AA965960
VERSION
AA965960.1 GI:3139844
KEYWORDS
EST.
SOURCE
Emericella nidulans.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
REFERENCE
1 (bases 1 to 227)
Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
Prade, R. and Roe, B.
An Aspergillus nidulans EST Database
unpublished (1998)
CONTACT: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: SK
High quality sequence stop: 153.

FEATURES

source

Location/Qualifiers
1..227
/organism="Emericella nidulans"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="r8a05a1"
/clone_1lb="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 40 a 65 c 74 g 48 t

Query Match 49.0%; Score 178.8; DB 9; Length 227;
Best Local Similarity 94.8%; Pred. No. 4.6e-34;
Matches 218; Conservative 0; Mismatches 7; Indels 5; Gaps 3;

Oy	36	gatagaagaacgcagaggaactcgataaagaatgtaatt-gcaagattcagtaacac	94
Db	1	GATGAGAAACCGACGGAAGCTGGATAGAAATGTGTAATTCGACAAATTCAGTGAATCATC	60
Oy	95	gagcttcctgaacgcacatctgcgcgccctcgcgatactccgggggagcatgcctctgcgaagctc	154
Db	61	TGAGCTTTCGAGCGACAAATGGCGCCCCCGTGGCATTCGGGGGGGCAATGCTGTCCGAGCGTC	120
Oy	155	attctctgcctctcaagaccgcgacttgctgtgttgagtcctgcctcccccctccgggggaagcg	214
Db	121	ATTGCTGCCCTCAACCCCGGGCTGTGTGTGTGGTGTGCTGT---CCGCCCGGGGGACGGG	177
Oy	215	cccgaaagcgacgcgcgcgcacgcg-ctcggctccctcgcagcgtatggagctc	263
Db	178	CCCGAAAGGACACGGCGGACACGATGCTCCGATCTTCGACCGATATGGGGTTT	227

RESULT	4
AA783772	189 bp mRNA linear EST 29-JUL-1998
LOCUS	
DEFINITION	c7g08a1.t1 Aspergillus nidulans 24hr asexual developmental and

ACCESSION	AA783772
VERSION	AA783772.1
KEYWORDS	GI:2843940
SOURCE	EST.
ORGANISM	<i>Emericella nidulans</i> . <i>Emericella nidulans</i>

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 189)
Kuefer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
Pride, R. and Roe, B.
An *Aspergillus nidulans* EST database
Unpublished (1998)

Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

FEATURES	Seq primer: SK.
source	Location/Qualifiers
	1..189
	/organism="Emerizella nidulans"
	/strain="FGSC A26"

/clone_11b-"Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="vector: pluescript SK-; site_1: EcoRI; site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pluescript

ORIGIN					
Query Match	40.98%	Score 149.2:	DB 9:	Length 189:	
Best Local Similarity	93.28%	Pred. No. 64e-27:			

0y 67 tctgatttcgaatcttcgattgatacatcagctcgtcttgaagcagacattcgcgccccctgga 126
 Db 1 tctgatttcgaatcttcgattgatacatcagctcgtcttgaagcagacattcgcgccccctgga 60
 0y 127 ttcgcgggggacatgaccttcaggagcatcttcctccctcaagcccgagcttfgtgg 186

QY	187	gctgtgtgtccccccccccgagagacgagcagcgcg -gtccggtc	245
Db	121	---gtctctctcccccccgaggacgagcccaaaagcagcggcgacacggtcc	177
QY	246	ctcgagcggtat	256
Db	178	ctcgcagcgtat	188

RESULT	5
CNS06XIS	882 bp DNA linear GSS 06-JUL-2001
LOCUS	T7 end of clone AY0AA01C10 of library AY0AA from strain CBS 6340
DEFINITION	of <i>Kluyveromyces thermotolerans</i> , genomic survey sequence.
ACCESSION	AF110786

KEYWORDS GSS.
SOURCE Kluveromyces thermotolerans.
ORGANISM Kluveromyces thermotolerans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluveromyces.
1 / 48803

TITLE	JOURNAL	DATE	ISSN	DOI
and Dujon, B. Genomic exploration of the hemiascomycetous yeasts: 10. Kluyveromyces thermotolerans FEMS Lett. 487 (1), 61-65 (2000) 20584720		14-03-2000	0167-7013	10.1016/S0167-7013(00)00050-1

Boletini-Pukuitara, M., Bon, E., Brottier, P., Casaregola, S., De-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B., Maltrepierre, M., Neugebisse, C., Ozier-Valogerosopoulos, O., Polier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
TONTANT
Submitted/04/05/2000] Copyright - Copyright Nacional] de Sciencia

COMMENT

sequelegenoscope.cns.it - Web : www.genoscope.cns.it

This GSS is part of a random genomic sequencing project of thirteen yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces fragilis*, *Kluyveromyces fragilis* var. *martyi*, *Rhodosporidium rubrum*.

FEATURES
source
1
882
location/qualifiers
the other extremity of this insert.
keywords for description of this sequence and for the sequence of
5 kb were prepared and both extremities were sequenced. See
Canada tropicalis and yarrowia lipolytica. Genomic inserts of 3 to
Canadia tropicalis and yarrowia lipolytica. Genomic inserts of 3 to

```
misc feature
1>882
/strain="CHS 6340"
/db_xref="taxon:4916"
/clone="AY0A001C10"
/clone_1lb="AY0AA"
/note="end : T7"
1>882
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Query Match	39.4%	Score 143.8	DR 12	Length 882
BASE COUNT	221 a	188 c	213 g	257 t
ORIGIN	/evidence-hol_experimental 3 others			

malines	103;	conservative	0;	mismatches	32;	indels	0;	gaps	0;
---------	------	--------------	----	------------	-----	--------	----	------	----

FEATURES	Source
REFERENCE	1117 bp DNA linear GSS 08-JUL-2001
LOCUS	CNS07ARF/6
DEFINITION	T3 end of clone BC0AA006C06 of library BC0AA from strain CBS 767 of Debaryomyces hansenii, genomic survey sequence.
ACCESSION	AL436945
VERSION	AL436945.1 GI:12220358
KEYWORDS	GSS.
SOURCE	Debaryomyces hansenii.
ORGANISM	Debaryomyces hansenii. Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.
REFERENCE	1 (bases 1 to 1117) Ledingue, A., Casaregola, S., Neuveglise, C., Bon, E., Nguyen, H., Artiguenave, F., Wincker, P. and Galliardin, C. Genomic exploration of the hemiascomycetous yeasts: 14. Debaryomyces hansenii var. hansenii FEBS Lett. 487 (1), 82-86 (2000)
TITLE	2 (bases 1 to 1117) Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G., Boitlot, P., Bon, E., Brothier, P., Casaregola, S., Delmotte, J., Dujon, B., Durieux, P., Ledingue, A., Lorente, B., Maupertuy, A., Neuveglise, C., Ozier, K., Pothier, S., Saurin, M., Tekala, F., Toffano-Nioche, C., Wesolowski, L., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
JOURNAL	20584711
MEDLINE	3 (bases 1 to 1117)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage
JOURNAL	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbophilophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES	location/Qualifiers
Source	1..1117 /organism="Debaryomyces hansenii" /strain="CBS 767" /variant="hansenii" /db_xref="taxon:4959" /clone="BC0AA006C06" /clone_11b="BC0AA" /note="end : T3"

misc_feature	<1..>1117	/note="part of rDNA repeats"
BASE COUNT	344 a 256 c 204 g 308 t	5 others
ORIGIN		
Query Match	39.0%: Score 142.2; DB: 12; Length 1117;	
Best Local Similarity	83.1%: Pred. No. 6.2e-25;	
Matches 162: Conservative	0; Mismatches 33; Indels 0; Gaps 0;	
Oy	1 aaacttaacaacatgatctcttgcttgcgcgcatcatgaaagaacgcagcaactgcgat 60	
Db	630 AAACCTTTAACACAGCAGATCTCTTGCTTCTCCGATCGATGAAGAACGCCAATATGCAT 571	
Oy	61 aagtaatgtaacatgtaacgaatcagtaacatcagatcagatcttgaacgacatctgcgcc 120	
Db	570 AAGTAATATGAAATTCACAGATTTTGCTGAATCATCATCAATCTTTGAACGCACATTTGGCCCT 511	
Oy	121 ctgcgcatccggggggatgcctctgcgcagcgcatactgcgcctcctaagccgcgctgtg 180	
Db	510 CTGGATTTTCAGAGGGCATGCGCTGTTTGAGCGTCATTTCTCTCAACATCTTGGGTTTGG 451	
Oy	181 tcttgatgcctgcgc 195	
Db	450 TATTTAGTGATATCTC 436	
RESULT 7	718 bp DNA Linear GSS 17-JUN-2001	
CNS06FTN/C	LOCUS	
DEFINITION	T7 end of clone XAR0A001B02 of library XAR0A from strain CBS 732	
ACCESSION	of Zygosaccharomyces rouxii, genomic survey sequence.	
VERSION	AL396849	
KEYWORDS	AL396849.1 GI:12149257	
SOURCE	GSS.	
ORGANISM	Zygosaccharomyces rouxii.	
REFERENCE	Zygosaccharomyces rouxii.	
AUTHORS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.	
TITLE	1 (bases 1 to 718)	
JOURNAL	de Montigny J., Straub M., Potier S., Tekala F., Dujon B.,	
MEDLINE	Wincker P., Artiguenave F. and Souciet J.	
REFERENCE	Zygosaccharomyces rouxii	
AUTHORS	FEBS Lett. 487 (1), 52-55 (2000)	
TITLE	2 (bases 1 to 718)	
JOURNAL	Souciet J. L., Aigle M., Artiguenave F., Blandin G.,	
MEDLINE	Boitot F., Fukuhara M., Bon E., Brothier P., Casaregola S.,	
REFERENCE	de Montigny J., Dujon B., Durand P., Lepingle A., Llorente B.,	
AUTHORS	Malpertuy A., Neuvéglise C., Ozier-Kalogeropoulos O., Potier S.,	
TITLE	Saurin M., Tekala F., Toffano-Nicolas C., Mesolowski-Louvel M.,	
JOURNAL	Wincker P. and Weissenbach J.	
MEDLINE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of	
REFERENCE	yeast species for molecular evolution studies	
AUTHORS	FEBS Lett. 487 (1), 3-12 (2000)	
TITLE	3 (bases 1 to 718)	
JOURNAL	Genoscope.	
MEDLINE	Direct Submission	
REFERENCE	Submitted (05-SEP-2000) Genoscope - Centre National de Séquençage.	
AUTHORS	2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
TITLE	This GSS is part of a random genomic sequencing program of thirteen	
JOURNAL	yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces	
MEDLINE	exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,	
REFERENCE	Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces	
AUTHORS	lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia	
TITLE	angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,	
JOURNAL	Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to	
MEDLINE	5 kb were prepared and both extremities were sequenced. See	
REFERENCE	keywords for description of this sequence and for the sequence of	

TITLE Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveglise,C., Olier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 889)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
 1..889
 /organism="Zygosaccharomyces rouxii"
 /strain="CBS 732"
 /db_xref="taxon:4956"
 /clone="AR0A013D02"
 /clone.lib="AR0A"
 /note="end : T3"
 /note="end : T3"
 misc_feature
 <1..>889
 /note="part of rDNA repeats
 contains 35S rDNA gene"
 /evidence="not_experimental"
 BASE COUNT 247 a 222 c 186 g 234 t
 ORIGIN

Query Match 38.7%; Score 141.4; DB 12; Length 889;
Best Local Similarity 93.1%; Pred. No. 9.4e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 aaacttcaacaatgatctcttggttcgcatcgatgaagaacgacgcaactgcgat 60
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 DB 648 AAACCTTCAACACGAGATCTCTTGTTCTCGATGTAAGAACGACGACATGGCAT 589
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 OY 61 aagtaatgtaattgcgaattcagtaatcagtcagtcatttgaacgacattggccccc 120
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 DB 588 ACCTAAATGTGAATTCGAGAAATTCGTAATCATCGAAATCTTTGAACGACATTTGCGCCC 529
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 OY 121 ctggcattccgggggcatgcctgctgcagcagcattatgc 159
 ||| ||||||||||| ||| ||||||||||| ||| ||||||||||| ||| |||||||||||
 DB 528 TTGGTATTCCGGGGGCGATGCTCTTTGAGCGTCATTTTC 490
 ||| ||||||||||| ||| ||||||||||| ||| ||||||||||| ||| |||||||||||

RESULT 12
CNS06CUX 902 bp DNA linear GSS 14-JUN-2001
LOCUS T7 end of clone AR0A008C01 of library AR0A from strain CBS 732 of
DEFINITION *Zygosaccharomyces rouxii*, genomic survey sequence.
ACCESSION AL393007
VERSION AL393007.1 GI:12142879
KEYWORDS GSS.
SOURCE *Zygosaccharomyces rouxii*.
ORGANISM *Zygosaccharomyces rouxii*.
REFERENCE 1 (bases 1 to 902)
AUTHORS de Montigny,J., Dujon,B., Durrens,P., Potier,S., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Soulet,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE 20584718
REFERENCE 2 (bases 1 to 902)
AUTHORS Soulet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveglise,C., Olier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 902)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
 1..902
 /organism="Zygosaccharomyces rouxii"
 /strain="CBS 732"
 /db_xref="taxon:4956"
 /clone="AR0A008C01"
 /clone.lib="AR0A"
 /note="end : T7"
 /note="end : T7"
 misc_feature
 <1..>902
 /note="part of rDNA repeats
 contains 35S rDNA gene"
 /evidence="not_experimental"
 BASE COUNT 236 a 191 c 220 g 254 t 1 others
 ORIGIN

Query Match 38.7%; Score 141.4; DB 12; Length 902;
Best Local Similarity 93.1%; Pred. No. 9.4e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 aaacttcaacaatgatctcttggttcgcatcgatgaagaacgacgcaactgcgat 60
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 DB 226 AAACCTTCAACACGAGATCTCTTGTTCTCGATGTAAGAACGACGACATGGCAT 285
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 OY 61 aagtaatgtaattgcgaattcagtaatcagtcagtcatttgaacgacattggccccc 120
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
 DB 286 ACCTAAATGTGAATTCGAGAAATTCGTAATCATCGAAATCTTTGAACGACATTTGCGCCC 345
 ||| ||||||||||| ||| ||||||||||| ||| ||||||||||| ||| |||||||||||

OY 121 ctggcattccgggggcatgcctgctgcagcagcattatgc 159
 ||| ||||||||||| ||| ||||||||||| ||| ||||||||||| ||| |||||||||||
 DB 346 TTGGTATTCCGGGGGCGATGCTCTTTGAGCGTCATTTTC 384
 ||| ||||||||||| ||| ||||||||||| ||| ||||||||||| ||| |||||||||||

RESULT 13
CNS06F06 928 bp DNA linear GSS 17-JUN-2001
LOCUS T7 end of clone XAR0A001C01 of library XAR0A from strain CBS 732
DEFINITION *Zygosaccharomyces rouxii*, genomic survey sequence.
ACCESSION AL396868
VERSION AL396868.1 GI:12149277
KEYWORDS GSS.
SOURCE *Zygosaccharomyces rouxii*.

ORGANISM Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

REFERENCE 1 (bases 1 to 928)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Souciet,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE 20584718
REFERENCE 2 (bases 1 to 928)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 928)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
LOCATION/Qualifiers

FEATURES
source 1..928
/organism="Zygosaccharomyces rouxii"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="XAR0A001C01"
/clone_lib="XAR0A"
/note="end : T7"
/note="end : T7"
misc_feature <1..>928
/note="part of rDNA repeats
contains 35S rDNA gene"
/evidence-not_experimental

BASE COUNT 251 a 187 c 230 g 258 t 2 others
ORIGIN

Query Match 38.7%: Score 141.4; DB 12; Length 928;
Best Local Similarity 93.1%: Pred. No. 9.5e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 aaacttcaacaatgatctctctgttccggatcagatgaagaacgacgaactgcgat 60
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DB 152 AAACCTTCAACACGATCTCTGTTCTCGCATGATGAAGACGACGAACCTGCAT 211
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QY 61 aagtaatgtaattgcagaatcagtgatcatcagatcttgaagcagatgcgcc 120
|||||
DB 212 ACCTGATGTGAATTCGCAATTCCTGTAATCATTCGAATCTTTGAACGACATTCGGCCCC 271
|||||
QY 121 ctggcatccgggggacatgcctgcgcagacgcatcgc 159
|||||
DB 272 TTGATATTCGGGGGCGATGCTGTTCAGCGTCATTTTC 310
|||||

RESULT 14
CNS06CB4/C
LOCUS CNS06CB4 936 bp DNA linear GSS 14-JUN-2001

DEFINITION T3 end of clone AR0A003E10 of library AR0A from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL392294
VERSION AL392294.1 GI:12141507
KEYWORDS GSS.
SOURCE Zygosaccharomyces rouxii.
ORGANISM Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

REFERENCE 1 (bases 1 to 936)
AUTHORS de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Souciet,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
JOURNAL FEBS Lett. 487 (1), 52-55 (2000)
MEDLINE 20584718
REFERENCE 2 (bases 1 to 936)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 936)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
LOCATION/Qualifiers

FEATURES
source 1..936
/organism="Zygosaccharomyces rouxii"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="AR0A003E10"
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/note="end : T3"
/note="end : T3"
misc_feature <1..>936
/note="part of rDNA repeats
contains 35S rDNA gene"
/evidence-not_experimental

BASE COUNT 266 a 227 c 188 g 245 t 10 others
ORIGIN

Query Match 38.7%: Score 141.4; DB 12; Length 936;
Best Local Similarity 93.1%: Pred. No. 9.5e-25;
Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 aaacttcaacaatgatctctctgttccggatcagatgaagaacgacgaactgcgat 60
|||||
DB 649 AAACCTTCAACACGATCTCTGTTCTCGCATGATGAAGACGACGAACCTGCAT 590
|||||
QY 61 aagtaatgtaattgcagaatcagtgatcatcagatcttgaagcagatgcgcc 120
|||||
DB 589 ACCTGATGTGAATTCGCAATTCCTGTAATCATTCGAATCTTTGAACGACATTCGGCCCC 530
|||||
QY 121 ctggcatccgggggacatgcctgcgcagacgcatcgc 159
|||||

Db 529 TTGGTATCCGGGGGCATGCTGTTTGAGCGTCATTTTC 491

RESULT 15

CNS06FXB 960 bp DNA linear GSS 17-JUN-2001

LOCUS T7 end of clone XAR0AA001H11 of library XAR0AA from strain CBS 732

DEFINITION of Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL396981

VERSION AL396981.1 GI:12149473

KEYWORDS GSS.

SOURCE Zygosaccharomyces rouxii.

ORGANISM Zygosaccharomyces rouxii

REFERENCE 1. de Montigny, J., Straub, M., Potier, S., Tekala, F., Dujon, B., Wincker, P., Artiguenave, F. and Souciet, U. Genomic exploration of the hemiascomycetous yeasts: 8. Zygosaccharomyces rouxii

AUTHORS

TITLE

JOURNAL FEBS Lett. 487 (1), 52-55 (2000)

MEDLINE 20584718

REFERENCE 2 (bases 1 to 960)

AUTHORS Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Boloiti, P., Fukuhara, M., Bon, E., Brotlier, P., Casaregola, S., de Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvéglise, C., Ozier-Kalogeropoulos, O., Polier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 3 (bases 1 to 960)

AUTHORS

TITLE Genoscope.

JOURNAL Direct Submission

MEDLINE Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)

REFERENCE This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

COMMENT

FEATURES

source

1. 960

/organism="Zygosaccharomyces rouxii"

/strain="CBS 732"

/db_xref="taxon:4956"

/clone="XAR0AA001H11"

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/note="end : 77"

<1..>960

/misc_feature

/note="part of rDNA repeats contains 35S rDNA gene"

/evidence="not_experimental"

BASE COUNT 254 a 198 c 237 g 270 t 1 others

ORIGIN

Query Match 38.7%; Score 141.4; DB 12; Length 960;

Best Local Similarity 93.1%; Pred. No. 9.5e-25;

Matches 148; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 aaacttcaacatgagatctcttggttcgcgatgatgaagaacgacgaactgcgat 60

|||||

Db 222 AACCTTTCAACACGAGATCTTGGTTCTCGATCGATGAGAACGACGACGAACCTGCAT 281

OY 61 aagtaatcgaattgcgaagaattcgaatcatcatcagtcctttgaaacgacacatgcgcgcc 120

|||||

Db 282 ACGTATCTGAATTGCAGAAATTCCTGATCATCATGCAATCTTTGAACGCACATTTCCGCCCC 341

OY 121 ctggcattcgcgggggacatgcctctgtccgagcgtcatcgc 159

|||||

Db 342 TTGGTATCCGGGGGCATGCTGTTTGAGCGTCATTTTC 380

Search completed: August 21, 2002, 21:32:05

Job time: 12504 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 20:37:27 ; Search time 138.45 Seconds

(without alignments)
647.571 Million cell updates/sec

Title: US-10-046-955-5
Perfect score: 365
Sequence: 1 aaacttcacaacatgctc.....gggataccgcgtgacttaa 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	70.1	556	4 US-09-037-9908-7	Sequence 7, Appl
2	220.6	60.4	498	4 US-09-037-9908-6	Sequence 6, Appl
3	206.8	56.7	611	3 US-08-986-727-4	Sequence 4, Appl
4	203.8	55.8	568	3 US-08-986-727-5	Sequence 5, Appl
5	188.4	51.6	608	3 US-08-986-727-3	Sequence 3, Appl
6	180.6	49.5	597	1 US-08-742-023-3	Sequence 3, Appl
7	180.6	49.5	597	3 US-08-968-505-3	Sequence 3, Appl
8	180.2	49.4	561	1 US-08-905-314A-24	Sequence 24, Appl
9	174.4	47.8	590	4 US-09-026-601-41	Sequence 41, Appl
10	171.8	47.1	531	1 US-08-652-127C-7	Sequence 7, Appl
11	171	46.8	583	1 US-08-652-127C-8	Sequence 8, Appl
12	171	46.8	2293	4 US-09-645-073-1	Sequence 6, Appl
13	170.8	46.8	581	4 US-08-652-127C-6	Sequence 6, Appl
14	170.4	46.7	579	4 US-09-026-601-38	Sequence 38, Appl
15	169.6	46.5	580	4 US-09-026-601-37	Sequence 37, Appl
16	169.2	46.4	579	4 US-09-026-601-29	Sequence 29, Appl
17	169.2	46.4	579	4 US-09-026-601-30	Sequence 30, Appl
18	169.2	46.4	579	4 US-09-026-601-34	Sequence 34, Appl
19	169.2	46.4	579	4 US-09-026-601-36	Sequence 36, Appl
20	168.8	46.2	579	4 US-09-026-601-32	Sequence 32, Appl
21	168	46.0	580	4 US-09-026-601-40	Sequence 40, Appl
22	167.6	45.9	545	2 US-08-722-187-85	Sequence 85, Appl
23	167.6	45.9	545	5 PCT-US95-04712-85	Sequence 85, Appl
24	167.2	45.8	579	4 US-09-026-601-31	Sequence 31, Appl
25	166.8	45.7	588	1 US-08-742-023-5	Sequence 5, Appl
26	166.8	45.7	588	3 US-08-968-505-5	Sequence 5, Appl
27	166.6	45.6	580	4 US-09-026-601-33	Sequence 33, Appl

28	166.4	45.6	588	1 US-08-742-023-4	Sequence 4, Appl
29	166.4	45.6	588	3 US-08-968-505-4	Sequence 4, Appl
30	166.4	45.6	594	1 US-08-652-127C-5	Sequence 5, Appl
31	165.8	45.4	548	1 US-08-233-608-1	Sequence 1, Appl
32	165.8	45.4	548	1 US-08-887-480-1	Sequence 1, Appl
33	165.8	45.4	548	2 US-08-722-187-1	Sequence 1, Appl
34	165.8	45.4	548	5 PCT-US95-04712-1	Sequence 1, Appl
35	165.6	45.4	556	1 US-08-887-480-85	Sequence 85, Appl
36	165.6	45.4	556	1 US-08-905-314A-23	Sequence 23, Appl
37	165.4	45.3	626	1 US-08-233-608-3	Sequence 3, Appl
38	165.4	45.3	626	2 US-08-887-480-3	Sequence 3, Appl
39	165.4	45.3	626	2 US-08-722-187-3	Sequence 3, Appl
40	165.4	45.3	626	4 US-09-635-747-38	Sequence 38, Appl
41	165.4	45.3	626	5 PCT-US95-04712-3	Sequence 3, Appl
42	165	45.2	546	1 US-08-887-480-96	Sequence 96, Appl
43	165	45.2	546	1 US-08-905-314A-22	Sequence 22, Appl
44	165	45.2	605	3 US-08-968-727-1	Sequence 1, Appl
45	163.8	44.9	534	1 US-08-233-608-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-037-9908-7
; Sequence 7, Application US/090379908
; Patent No. 6248519
; GENERAL INFORMATION:
; APPLICANT: ENGEL, Stacia R.
; DESCENZO, Richard A.
; MORENZONI, Richard A.
; IRELAN, Nancy A.
; TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED MICROORGANISMS
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,9908
; FILING DATE: 11-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 29520/30001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 556 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-037-9908-7

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-986-727-4

Query Match 56.7%; Score 206.8; DB 3; Length 611;
Best Local Similarity 76.8%; Pred. No. 2,9e-53;
Matches 281; Conservative 0; Mismatches 77; Indels 8; Gaps 2;

QY 1 aaattcaacaatgatgctcttggcttcggacatcagatgaagaacgacgaactgcgat 60
DB 232 AAATTTCACCAACGATCTCTGTGCTTGCGATCATGAAAGCAGCAAGAAATCGCAT 291
QY 61 aagtaatgtaattgcgaattcagtgatcatcagtcgtcttgaagcaattgcgccc 120
DB 292 AAGTAATGTAATTGCGAATTCAGTGAATCATGAAATCTTGAAGCAGCAATGCGCCT 351
QY 121 ctggacatccgggggagcagctctgcagagcgatcattgtctgcctcaagccgagcttg 180
DB 352 CTGGTATTCGGAGGCGATGCTGTTCGAGCGTCATTTCAACCCCTCAAGCCTGGCTTG 411
QY 181 tgttggtcgtctgctcccccgggggagcagccgaaagcagcgagcgacagctgc 240
DB 412 GATGGGCGACTGCTCCCGCCCGGGGAGCGAGGCGCTGAATCACTGAGCGAGCTG--- 468
QY 241 cggctcagcgatgagggctgtgacccgctcagatlaagggcgccgggagcgccagcc 300
DB 469 ----CCAGGAGCCCGAGCGAGTGAATCAACCTCGCTCCGGAGAGCCCTGGCGGTGCC 524
QY 301 ggcgctcacaactatcctt-tctcaggttgacctgcagtcagtgagataccgcctga 359
DB 525 TGCCGTTAAACCCCAACTTGTGAAGTTGACCTCGATGAGTGAATACCCGCTGA 584
QY 360 acttaa 365
DB 585 ACTTAA 590

RESULT 4
US-08-986-727-5

; Sequence 5, Application US/08986727
; Patent No. 6080543
; GENERAL INFORMATION:
; APPLICANT: ENGEL, Stacia R.
; APPLICANT: DESCENZO, Richard A.
; APPLICANT: IRELAN, Nancy A.
; TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,727
; FILING DATE: 08-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ekstrom, Richard C.
; REGISTRATION NUMBER: 37,027
; REFERENCE/DOCKET NUMBER: 009773-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-986-727-5

Query Match 55.8%; Score 203.8; DB 3; Length 568;
Best Local Similarity 76.4%; Pred. No. 2,2e-52;
Matches 279; Conservative 0; Mismatches 77; Indels 9; Gaps 2;

QY 1 aaattcaacaatgatgctcttggcttcggacatcagatgaagaacgacgaactgcgat 60
DB 191 AAATTTCACCAACGATCTCTGTGCTTGCGATCATGAAAGCAGCAAGAAATCGCAT 250
QY 61 aagtaatgtaattgcgaattcagtgatcatcagtcgtcttgaagcaattgcgccc 120
DB 251 AAGTAATGTAATTGCGAATTCAGTGAATCATGAAATCTTGAAGCAGCAATGCGCCT 310
QY 121 ctggacatccgggggagcagctctgcagagcgatcattgtctgcctcaagccgagcttg 180
DB 311 TTGATATTCGGGCGGCGATGCTGTTCGAGCGTCATTAACACCTCAAGCCTGCTGTTG-- 368
QY 181 tgttggtcgtctgctcccccgggggagcagccgaaagcagcgagcgacagctgc 240
DB 369 ----CAATTTGGGACCGTCTCTACGTCGAGCGCGCTCGAAGACCTCGCGGTGCTGTT 424
QY 241 cggctcagcgatgagggctgtgacccgctcagatlaagggcgccgggagcgccagcc 300
DB 425 CAGCCCTCAGCGTGTGTAATACACCTCGCTTGAGATGTTGGCGTGGCCCGGAC 484
QY 301 ggcgctcacaactatccttctcaggttgacctgcagtcagtgagataccgcctga 360
DB 485 GAACCTCTGAACCTTTCT---CAAGGTTGACCTCGATGAGTGAATACCCGCTGA 541
QY 361 cttaa 365
DB 542 CTTAA 546

RESULT 5
US-08-986-727-3

; Sequence 3, Application US/08986727
; Patent No. 6080543
; GENERAL INFORMATION:
; APPLICANT: ENGEL, Stacia R.
; APPLICANT: DESCENZO, Richard A.
; APPLICANT: IRELAN, Nancy A.
; TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,727
; FILING DATE: 08-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ekstrom, Richard C.
; REGISTRATION NUMBER: 37,027
; REFERENCE/DOCKET NUMBER: 009773-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620


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NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..181
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note="5' end of large subunit
US-08-905-314A-24
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Query Match 49.4% Score 180.2; DB 1; Length 561;
Best Local Similarity 71.8%; Pred. No. 2.8e-45;
Matches 265; Conservative 2; Mismatches 90; Indels 12; Gaps 2;
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QY 1 aaacttcaacatgagatctctgtgtccgacatgagaagacagcagcagatcgat 60
DB 181 AACTTTCAACAGCATCTCTGTGTTCTGCGATGATGAAGAACGACGAATGCGAT 240
QY 61 aagtaatgtaattcgagaattcagtgaaatcagatcagatcgttgaagcagatcgccc 120
DB 241 AAGTAATGTGAATTCAGAAATTCAGTAATCAGTAATCTTTGAACGACATTCGCCCG 300
QY 121 ctggcattccgggggagatgctgtccgacatgctgctgcccctgaagccc-----gact 176
DB 301 CTGGTATTCCCGCGGCGATGCTGTTGAGCGTCAATTTCAACCTCAAGCCCGCGGTTT 360
QY 177 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 236
DB 361 GGTGTGGGGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 237 gttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 296
DB 421 G-----CTGCAGCCTCCATTCCTGTAAGTAAACACCTCCCACTCGAAGCGCGCGC 472
QY 297 agccgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 356
DB 473 GGCATGCGGTAAGACCCCAATTCGTAATGTGACCTCGATCAGGTAGGAATACCCCGC 532
QY 357 tgaacttaa 365
DB 533 TGAACTTAA 541
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RESULT 9
US-09-026-601-41
Sequence 41, Application US/09026601
Patent No. 6358680
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: Detection of Wheat and Barley Fungal
TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6358680artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6358680th Carolina
COUNTRY: USA
ZIP: 27709
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,601
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1984
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Pyrenophora teres
INDIVIDUAL ISOLATE: 36570
IMMEDIATE SOURCE:
CLONE: 10-1
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..209
OTHER INFORMATION: /note="ITS1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 210..366
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 367..536
OTHER INFORMATION: /note="ITS2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 537..590
OTHER INFORMATION: /note="5' end of large subunit"
US-09-026-601-41
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Query Match 47.8% Score 174.4; DB 4; Length 590;
Best Local Similarity 70.9%; Pred. No. 1.6e-43;
Matches 258; Conservative 1; Mismatches 102; Indels 3; Gaps 2;
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QY 2 aacttcaacatgagatctctgtgtccgacatgagaagacagcagcagatcgata 61
DB 210 AACTTTCAACAGCATCTCTGTGTTCTGCGATGATGAAGAACGACGAATGCGAT 269
QY 62 agtaatgtaattcgagaattcagtgaaatcagatcagatcgttgaagcagatcgccc 121
DB 270 ACTAGTGAATTCAGAAATTCAGTAATTCAGTAATTCAGTAATTCAGTAATTCAGTA 329
QY 122 tggcattccgggggagatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 181
DB 330 TGGTATTCGAAAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 388
QY 182 gttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 241
DB 389 GTTGGCGCTTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
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OY 242 ggtcctcagcgtatggtgcttgatccgcgtcagttagggccggcgagccagccg 301
DB 449 TGTGTTTCGGAGCCGACACATTTATTTGCGCTTGTTCAGCCCGCGTCCGCGCTC--CAT 506
OY 302 ggcctcccaacctatcttctcaggttgacctcgatcaggttaggtatcccgctgaac 361
DB 507 GAAGCCTTTTTTTTTTTTTCAGCCTTTTGACTCTCGGATCAGTAGGAGATACCCGCTGAAC 566
OY 362 ttaa 365
DB 567 TTAA 570

RESULT 10
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5815
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-7

Query Match 47.1%; Score 171.8; DB 1; Length 531;
Best Local Similarity 72.4%; Pred. No. 9.4e-43;
Matches 267; Conservative 0; Mismatches 89; Indels 13; Gaps 3;
OY 1 aaacttcaacaatgagatctctgtgtccgcatcagatgaagaacgagcaactgcgat 60
DB 152 AAACCTTCAACAACGAGATCTCTGTGTCGATCGATGAAAGCAAGCAAGAAATGCGAT 211
OY 61 aagtaagtgaattgcagaattcaagtgatcatcagagctcttgaagcacatgtgcgcc 120
DB 212 AAGTAATGTGAATTTGCAAGATTCAGTGAATCATCGAATCTTTGAACGACACATTGCCCG 271
OY 121 ctggcattccgggggagatcctgtccgagcgtcatgtgcctccaagccc-----gact 176
DB 272 CCAATATCTTGGCGGCGATCCTGTTGAGCGTCAATTTCAACCCCTCAAGCCCGGGCTT 331
OY 177 tgtgtgttggtcgtcgtcccccgggggagcgagcccgaaagcagcgagcgacac 236
DB 332 GGTGTGAGATAGCGTCCGCCCGGGCGCGCCGCTCTTAATAATATAGTGCGCGTCTC 391

OY 237 gttccggtcctcagcgtatggtgcttgatccgcgtcagttagggccggcgagccg 296
DB 392 G-----CTGTAGCTCTCTCGGTAGTAGACACCTCCGACATGGAACACGCGCGC 443
OY 297 agcggcgtctccacctatcttctcaggttgacctcgatcaggttaggtatcccg 356
DB 444 -CACGCCGTTAAACCCCGCACTTGTGAAGAGTTGACCTCGATCAGTAGAATAACCGC 502
OY 357 tgaactaa 365
DB 503 TGAATTAA 511

RESULT 11
US-08-652-127C-8
; Sequence 8, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; ADDRESS: Seaby & Maclean
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5815
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match 46.8%; Score 171; DB 1; Length 583;
Best Local Similarity 72.5%; Pred. No. 1.7e-42;
Matches 266; Conservative 0; Mismatches 90; Indels 11; Gaps 3;
OY 1 aaacttcaacaatgagatctctgtgtccgcatcagatgaagaacgagcaactgcgat 60
DB 206 AAACCTTCAACAACGAGATCTCTGTGTCGATCGATGAAAGCAAGCAAGAAATGCGAT 265
OY 61 aagtaagtgaattgcagaattcaagtgatcatcagagctcttgaagcacatltgcgcc 120
DB 266 AAGTAATGTGAATTTGCAAGATTCAGTGAATCATCGAATCTTTGAACGACACATTGCCCG 325
OY 121 ctggcattccgggggagatcctgtccgagcgtcatgtgcctccaag-----ccggctg 178
DB 326 CTAGTATTTCTGGCGGCGATCCTGTTGAGCGTCAATTTCAACCCCTCAAGCCCGGGCTT 385
OY 179 tgtgtgttggtcgtcgtcccccgggggagcgagcccgaaagcagcgagcgacac 238

Db 386 GGTGTGGGATGGGAGCGCTCGCGCCGCCCTCCCTAAATCTAGTGGCGTCTCG- 444
Oy 239 tccggtccctcagcgcgtatggggttggttcacccgctcgtatgaagccggcgccgca 288
Db 445 -----CTGTAGCTTCTCTCTGTAGTACACACTCGACATGGGAAACAGCGCGC-C 496
Oy 299 ccggcgctcccaaccatctcttcaggttcaggttcaggttcaggttcaggttcaggttc 358
Db 497 ACGCCGTTAAACCCCAACTTCTGAAGTTTGACCTCGATCAGTACGATGGAATACCCGCTG 556
Oy 359 aacttaa 365
Db 557 AACTTAA 563

RESULT 12
US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; TITLE OF INVENTION: Production of High Titters of Glibdrellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; PRIORITY FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Glibdrellia fulvikuroi
US-09-645-073-1

Query Match 46.8%; Score 171; DB 4; Length 2293;
Best Local Similarity 70.6%; Pred. No. 2.8e-42;
Matches 259; Conservative 0; Mismatches 100; Indels 8; Gaps 2;
Oy 1 aaacttcaacaatgagatctcttggttcgagcagtcagatgaagaagcagcgaactcgat 60
Db 1921 aaacttcaacaagagatctcttggttcgagcagtcagatgaagaagcagcgaactcgat 1980
Oy 61 aagtaatgagatgagcagatcagatcagatcagatcagatcagatcagatcagatcagat 120
Db 1981 aagtaatgagatgagcagatcagatcagatcagatcagatcagatcagatcagatcagat 2040
Oy 121 ctggaatccgggggagcagtcgcttcgagcagtcagatcagatcagatcagatcagatcagat 178
Db 2041 ccagatctctggtgggagcagtcgcttcgagcagtcagatcagatcagatcagatcagatcagat 2100
Oy 179 tctgtgtggtcgtctcgtcccccgggggagcgggcccgaagcagcggcgagcagcgg 238
Db 2101 ggtgtgtggtcgtctcgtcccccgggggagcgggcccgaagcagcggcgagcagcgg 2160
Oy 239 tccggtccctcagcgcgtatggggttggttcacccgctcgtatgaagccggcgccgca 298
Db 2161 ctggaatccgggggagcagtcgcttcgagcagtcagatcagatcagatcagatcagatcagat 2214
Oy 299 ccggcgctcccaaccatctcttcaggttcaggttcaggttcaggttcaggttcaggttcaggttc 358
Db 2215 caagcgcttaaacccccaacttctgaatggtgacctcgtatcagatcagatcagatcagatcagat 2274
Oy 359 aacttaa 365
Db 2275 aacttaa 2281

RESULT 13
US-08-652-127C-6
; Sequence 6, Application US/08652127C

; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-652-127C-6

Query Match 46.8%; Score 170.8; DB 1; Length 581;
Best Local Similarity 72.1%; Pred. No. 1.9e-42;
Matches 266; Conservative 1; Mismatches 89; Indels 13; Gaps 3;
Oy 1 aaacttcaacaatgagatctcttggttcgagcagtcagatgaagaagcagcgaactcgat 60
Db 202 AAACCTTCAACAGGATCTCTGTGTCGATCATGATGAAGCAGCAATTCGCGAT 261
Oy 61 aagtaatgagatgagcagatcagatcagatcagatcagatcagatcagatcagatcagat 120
Db 262 AAGTAATGTAATGCAAGATTCAGTGAATCATCGAATCTTTGAACGACATTCGCGCG 321
Oy 121 ctggaatccgggggagcagtcgcttcgagcagtcagatcagatcagatcagatcagatcagat 176
Db 322 CCAAGTATTCGGGGGAGGATGCTGTGTCGACGTCATTTCAACCTCAACCCCGGCGTT 381
Oy 177 tctgtgtggtcgtctcgtcccccgggggagcgggcccgaagcagcggcgagcagcgg 236
Db 382 GGTGTGGAAGATGGGCTGCCCGCGGCGGCGCCNSCTCCCAAAATATGATGCGGTCTC 441
Oy 237 ggtcgtccctcagcgcgtatggggttggttcacccgctcgtatgaagccggcgccgca 296
Db 442 G-----CTGTAGCTTCTCTCTGTAGTACACACTCGACATGGGAAACAGCGTGGC 493
Oy 297 ccggcgctcccaaccatctcttcaggttcaggttcaggttcaggttcaggttcaggttcaggttc 356
Db 494 -CACGCCGTTAAACCCCAACTTCTGAAGTTTGACCTCGATCAGTACGATGGAATACCCCGC 552
Oy 357 tgaacttaa 365
Db 553 TGAACCTAA 561

RESULT 14
US-09-026-601-38

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: Sequence 38, Application US/09026601
: Patent No. 6358680
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: Detection of Wheat and Barley Fungal
: TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6358680artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6358680th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,601
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1984
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 38:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 579 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Pyrenophora tritici-repentis
: INDIVIDUAL ISOLATE: 407
: IMMEDIATE SOURCE:
: CLONE: 7-3-2
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note="3' end of small subunit"
: OTHER INFORMATION: rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 31..208
: OTHER INFORMATION: /note="ITS1"
: FEATURE:
: NAME/KEY: misc_feature
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: OTHER INFORMATION: /note="5.8S rRNA gene"
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: NAME/KEY: misc_feature
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: OTHER INFORMATION: /note="ITS2"
: NAME/KEY: misc_feature
: LOCATION: 527..579
: OTHER INFORMATION: /note="5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
: US-09-026-601-38
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: Query Match 46.7%; Score 170.4; DB 4; Length 579;
: Best Local Similarity 70.9%; Pred. No. 2,6e-42;
: Matches 258; Conservative 1; Mismatches 92; Indels 13; Gaps 2;
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: 2 aacttcaacatgagatctctgtgtccgacatgataaagacgacgacatcgata 61
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```

Db 209 AACTTCAACACGATCTCTGTTCGTCATGCATGAAGAACGACGCAATGCATGA 268
Qy 62 agtaatgtaattgcgaattcagtaatcagtcagtccttgaacgcacattgcgc 121
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Db 269 AGAGTGTGAATTCAGAAATTCAGTAATTCAGTAATTCAGTAATTCAGTAATTC 328
Qy 122 tgcattccgggggagatcctcgtccgaacgcatctgcgccttaacgcgcgttgc 181
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Qy 182 gtgggtcgtcgtcccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 241
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 TTGGGGGTCTGTCTCTCTCC---GAGACTGCGCTTAATCATTTGCGACGCGGCT 445
Qy 242 ggtcctcgaagcgtatgagcgttgatccgcgtcgattgagcgcgcgcgcgcgc 301
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 446 TGGTTTCGAGCGACACACATTTATTTGCGCTGTTCGACGCGCTCG-----C 495
Qy 302 ggcgtcccaacctatccttcagtgatcagtcagtcagtcagtcagtcagtcagtc 361
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 GCGTCCATGACGCTTTTCACCTTTGACCTGAGATGAGGATACCGCTGAC 555
Qy 362 ttaa 365
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Db 556 TTA 559
:
: RESULT 15
: US-09-026-601-37
: Sequence 37, Application US/09026601
: Patent No. 6358680
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: Detection of Wheat and Barley Fungal
: TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6358680artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: No. 6358680th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,601
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1984
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8587
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 580 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Pyrenophora tritici-repentis
: INDIVIDUAL ISOLATE: 109
: IMMEDIATE SOURCE:
: CLONE: 6-2
: FEATURE:
: NAME/KEY: misc_feature

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Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:01:55 ; Search time 8184.59 Seconds

(without alignments)
964.830 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-10-046-955-5
365
1 aaacttcacacatgatctc.....gggataccgcgtgaacttaa 365

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
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26: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
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Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	365	100.0	365	18 US-09-423-233-5	Sequence 5, Appl1
2	334.8	91.7	565	12 US-09-580-797-36	Sequence 36, Appl1
3	334.8	91.7	9143	18 US-09-404-520-5563	Sequence 5963, Ap
4	333.2	91.3	438	52 US-60-132-861-8175	Sequence 8175, Ap
5	333.2	91.3	568	52 US-60-132-861-7761	Sequence 7761, Ap
6	332.2	91.0	574	52 US-60-132-861-10156	Sequence 10156, A
7	321.8	88.2	642	22 US-09-580-797-6	Sequence 6, Appl1
8	316	86.6	381	52 US-60-132-861-7287	Sequence 7287, Ap
9	308.2	84.4	551	52 US-60-132-861-9331	Sequence 9331, Ap
10	306.4	83.9	559	22 US-09-580-797-37	Sequence 37, Appl
11	299.8	82.1	552	18 US-09-580-797-39	Sequence 39, Appl
12	298.4	80.4	646	22 US-09-404-520-17184	Sequence 17184, A
13	284.2	77.9	365	18 US-09-580-797-3	Sequence 3, Appl1
14	279.8	76.7	7997	47 US-60-082-300-11599	Sequence 11599, A
15	278.2	76.2	597	22 US-09-580-797-35	Sequence 35, Appl
16	273.8	75.0	359	22 US-09-580-797-37	Sequence 37, Appl
17	273	74.8	601	52 US-60-132-861-6688	Sequence 6688, Ap
18	272.6	74.7	700	22 US-09-580-797-30	Sequence 30, Appl
19	272	74.5	608	22 US-09-580-797-38	Sequence 38, Appl
20	265.2	72.7	674	22 US-09-580-797-7	Sequence 7, Appl1
21	260.8	71.5	676	22 US-09-580-797-5	Sequence 5, Appl1
22	259	71.0	685	22 US-09-580-797-4	Sequence 4, Appl1
23	258.8	70.9	344	18 US-09-580-797-34	Sequence 7, Appl1
24	256	70.1	556	14 US-09-423-233-2	Sequence 2, Appl1
25	256	70.1	556	14 US-09-423-233-2	Sequence 7, Appl1
26	252.8	69.3	595	22 US-09-580-797-34	Sequence 34, Appl
27	239.8	65.7	576	18 US-09-417-507-20902	Sequence 20902, A
28	239.8	65.7	672	22 US-09-580-797-8	Sequence 8, Appl1
29	230.4	63.1	355	18 US-09-423-233-4	Sequence 4, Appl1
30	230	63.0	850	18 US-09-404-520-17173	Sequence 17173, A
31	221.2	60.6	382	16 US-09-241-427-2	Sequence 2, Appl1

32	230.6	60.4	498	1	PCT-US99-04251.6	Sequence 6, Appl.
33	220.6	60.4	498	1	US-09-037-990-6	Sequence 6, Appl.
34	219.2	60.1	414	52	US-60-132-861-11629	Sequence 11,629,
35	212.8	58.3	654	22	US-09-580-797-26	Sequence 26, Appl.
36	212.8	58.3	700	22	US-09-580-797-16	Sequence 16, Appl.
37	210	56.7	692	22	US-09-580-797-17	Sequence 17, Appl.
38	206.8	56.7	611	1	PCT-US98-8-25210-0	Sequence 4, Appl.
39	203.6	55.6	39	09	US-09-423-233-08	Sequence 28, Appl.
40	203.6	55.6	39	18	US-09-423-233-08	Sequence 28, Appl.
41	201.8	55.8	568	1	PCT-US98-8-25210-0	Sequence 4, Appl.
42	196.4	53.3	451	52	US-60-132-861-4200	Sequence 4200, A
43	190.8	52.3	465	52	US-60-132-861-6561	Sequence 6561, A
44	190.8	52.3	714	22	US-09-580-797-31	Sequence 31, Appl.
45	188.4	51.6	608	1	US-60-132-861-8072	Sequence 8072, A
					PCT-US98-8-25210-0	Sequence 3, Appl.

ALIGNMENTS

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RESULT 1
US-09-423-233-5
: Sequence 5, Application US/09423233
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America as
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 03063-0341mp
: CURRENT APPLICATION NUMBER: US/09/423.233
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
: US-09-423-233-5

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Best Local Similarity	100.0%;	Pred. No. 1.1e-84;		
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Qy	1	aaacttccaacaaatggaatctctctctgttcctcgagcatcgaatgaagaaacggaactgcat	60
Dp	1	aaacttccaacaaatggaatctctctctgttcctcgagcatcgaatgaagaaacggaactgcat	60
Qy	61	aagtaatgtgaaatctgcagaatctcagtgaatcatcatcgaatctctttgaacacatctgcgcc	120
Dp	61	aagtaatgtgaaatctgcagaatctcagtgaatcatcatcgaatctctttgaacacatctgcgcc	120
Qy	121	ctggacatctcgggggagcaatgcctgcgcgaacgctcatctgtccctcgaaccccgagctgtg	180
Dp	121	ctggacatctcgggggagcaatgcctgcgcgaacgctcatctgtccctcgaaccccgagctgtg	180
Qy	181	tgtttggggtcgtgcgtcccccgcgggggagacgggcccgaagaagagaggggcaacccgtc	240
Dp	181	tgtttggggtcgtgcgtcccccgcgggggagacgggcccgaagaagagaggggcaacccgtc	240
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Dp	301	ggcgctcccaacacttaacttctctcaaggttgacactcgaatcaaggtlaaggaataaccgctgaa	360
Qy	361	cttaa 365	
Dp	361	cttaa 365	

RESULT 2
US-09-580-797-36

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: General: 36 Application US/09580797
: GENERAL INFORMATION:
:
: APPLICANT: Iwen, Peter C.
: APPLICANT: Hinrichs, Steven H.
: APPLICANT: Henry, Travis
: TITLE OF INVENTION: Board of Regents of the University of Nebraska
: TITLE OF INVENTION: Materials and Methods for Molecular
: FILE REFERENCE: UNMC 63149
: CURRENT APPLICATION NUMBER: US/09/580,797
: CURRENT FILING DATE: 2000-05-30
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 36
:
: LENGTH: 565
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: TYPE: DNA
: ORGANISM: Aspergillus nidulans
: US-09-580-797-36

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Query Match	91.78;	Score 334.8;	DB 22;	Length 565;
Best Local Similarity	98.48;	Pred. No. 8.4e-77;		
Matches 360; Conservative	0;	Mismatches 2;	Indels 4;	Caps 2

[illegible]

RESULT

```

US-09-404-520-5963
: Sequence 5963, Application US/09404520
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Ghodssi, Azita
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: McInloch, James
: APPLICANT: Timberlake, William E.
: APPLICANT: Yu, Jaehyuk
: TITLE OF INVENTION: Emecella nidulans Genome Sequence and Uses Thereof
: FILE REFERENCE: 38-10(15498)A
: CURRENT APPLICATION NUMBER: US/09/404,520
: CURRENT FILING DATE: 1999-09-23
: NUMBER OF SEQ ID NOS: 44345
: SEQ ID NO 5963
: LENGTH: 9143
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
US-09-404-520-5963

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; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 13800
; SEQ ID NO 10156
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-132-861-10156
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Query Match          91.0%; Score 332.2; DB 52; Length 574;
Best Local Similarity 98.1%; Pred. No. 4e-76;
Matches 358; Conservative 0; Mismatches 3; Indels 4; Gaps 2;
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```

Qy 2 aacttcacaatgatactctgtgtccggatcgatgaagaacgacgaactgcgata 61
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Qy 62 agtaatgtaattcgaatattcgaatcgaatcgaatcgaatcgaatcgaatcgaat 121
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Db 105 agtaatgtaattcgaatattcgaatcgaatcgaatcgaatcgaatcgaatcgaat 164
Qy 122 tggcatccgggggagcgtcgtccgacgacgtcgtccgacgacgacgtcgtcgt 181
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 165 tggcatccgggggagcgtcgtccgacgacgtcgtccgacgacgacgtcgtcgt 224
Qy 182 gtgggtcgtcgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 240
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 gtgggtcgtcgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 281
Qy 241 cgggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy 301 ggggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 360
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 342 ggggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 401
Qy 361 cttaa 365
    | | | | |
Db 402 cttaa 406
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RESULT 7
US-09-580-797-6
; Sequence 6, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; APPLICANT: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-580-797-6
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Query Match          88.2%; Score 321.8; DB 22; Length 642;
Best Local Similarity 98.3%; Pred. No. 2.1e-73;
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```

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Qy 61 aagtaatgtaattcgaatattcgaatcgaatcgaatcgaatcgaatcgaatcgaat 120
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```

Db 353 aagtaatgtaattcgaatattcgaatcgaatcgaatcgaatcgaatcgaatcgaat 412
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Qy 121 tggcatccgggggagcgtcgtccgacgacgtcgtccgacgacgacgtcgtcgt 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 413 tggcatccgggggagcgtcgtccgacgacgtcgtccgacgacgacgtcgtcgt 472
Qy 181 tgggtgtcgtcgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 239
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 473 tgggtgtcgtcgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 529
Qy 240 cgggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 299
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 530 cgggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 589
Qy 300 cgggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 352
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 590 cgggtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 642
```

```

RESULT 8
US-60-132-861-7287
; Sequence 7287, Application US/60132861
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Timberlake, William E.
; TITLE OF INVENTION: ASPERGILLUS NIDULANS GENOME SEQUENCE AND USES THEREOF
; FILE REFERENCE: 38-21(15485)C
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 13800
; SEQ ID NO 7287
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-132-861-7287
```

```

Query Match          86.6%; Score 316; DB 52; Length 381;
Best Local Similarity 97.4%; Pred. No. 6.1e-72;
Matches 343; Conservative 0; Mismatches 5; Indels 4; Gaps 2;
```

```

Qy 15 ggaatcctgtgtccgacgacgacgacgacgacgacgacgacgacgacgacgacgac 74
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 ggaatcctgtgtccgacgacgacgacgacgacgacgacgacgacgacgacgacgac 60
Qy 75 ggaatcctgtgtccgacgacgacgacgacgacgacgacgacgacgacgacgacgac 134
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ggaatcctgtgtccgacgacgacgacgacgacgacgacgacgacgacgacgacgac 120
Qy 135 ggaatcctgtgtccgacgacgacgacgacgacgacgacgacgacgacgacgacgac 194
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 ggaatcctgtgtccgacgacgacgacgacgacgacgacgacgacgacgacgacgac 180
Qy 195 cccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 253
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 cccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtccgtcc 237
Qy 254 tatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 313
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 tatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 297
Qy 314 tatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 365
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 298 tatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 349
```

```

RESULT 9
US-60-132-861-9331/C
; Sequence 9331, Application US/60132861
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Timberlake, William E.
```



```

RESULT 12
US-09-580-797-3
: Sequence 3, Application US/09580797
: GENERAL INFORMATION:
: APPLICANT: Iwen, Peter C.
: APPLICANT: Hinchls, Steven H.
: APPLICANT: Henry, Travis
: TITLE OF INVENTION: Board of Regents of the University of Nebraska
: TITLE OF INVENTION: Materials and Methods for Molecular
: FILE REFERENCE: UMC 63149
: CURRENT APPLICATION NUMBER: US/09/580.797
: CURRENT FILING DATE: 2000-05-30
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 646
: TYPE: DNA
: ORGANISM: Aspergillus ustus
US-09-580-797-3

```

Query Match	80.4%;	Score 293.4;	DB 22;	Length 646;
Best Local Similarity	-96.6%;	Pred. No. 5.1e-66;		
Matches 343;	Conservative	0;	Mismatches 6;	Indels 6;
				Gaps 4;

[illegible]

```

RESULT 13
US-09-423-233-3
: Sequence 3, Application US/09423233
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America as
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 03063-0341mp
: CURRENT APPLICATION NUMBER: US/09/423.233
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 3
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus niger
: US-09-423-233-3

```

Query Match	77.98;	Score 284.2;	DB 18;	Length 365;
Best Local Similarity	91.38;	Pred. No. 1.2e-63;		

Matches 335; Conservative 0; Mismatches 28; Indels 4; Gaps 3.

QY	1	aaattccacaacatgga	tctctcttggttcctccggacatcgatggaagacgacgaatctgcgat	60
Db	1	aaattccacaacatgga	tctctcttggttcctccggacatcgatggaagacgacgaatctgcgat	60
QY	61	aagtaatgtaattgcagaa	atccagtgaaatcatcgaatctcttcttgaaacgcacatctgcgccc	120
Db	61	aagtaatgtaattgcagaa	atccagtgaaatcatcgaatctcttcttgaaacgcacatctgcgccc	120
QY	121	ctggacatccggggggc	atgcctgtccagacgtcattgtctgtccctcgaacgcggccttgctg	180
Db	121	ctggatctccggggggc	atgcctgtccagacgtcattgtctgtccctcgaacgcggccttgctg	180
QY	181	tgtttggctgcgtgcgt	cccccccccgcgggggaagcggcccgaaagacgaacgggcggacggcgc	238
Db	181	tgtttggctgcgtgcgt	cccccccccgcgggggaagcggcccgaaagacgaacgggcggacggcgc	240
QY	239	tcgcgctcctcgagcga	tatctggagctcttgatccacccgcctgcgaattaaagcccgggccggccgacg	298
Db	241	tcgcgctcctcgagcga	tatctggagctcttgatccacccgcctgcgaattaaagcccgggccggccgacg	298
QY	299	ccggcgtctccaaccta	ctttcttcacagcttgacactcgatcagtaggataaccgcctg	358
Db	299	ccggcgtctccaaccta	ctttcttcacagcttgacactcgatcagtaggataaccgcctg	358
QY	359	aacttaa	365	
Db	359	aacttaa	365	

RESULT 14
US-60-082-300-11599

GENERAL INFORMATION:
 APPLICANT: LAGACE, ROBERT E.
 APPLICANT: CORLEY, NELL C.
 APPLICANT: RUSSO, FRANK D.
 APPLICANT: HANN, AMY L.
 APPLICANT: HEATH, JOE D.
 APPLICANT: FINNEY, GREGORY L.
 APPLICANT: BROOKS, JACQUELINE
 TITLE OF INVENTION: NICOTINOTIDE SEQUENCES OF ASPERGILLUS FUNIGATUS
 TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
 NUMBER OF SEQUENCES: 21910
 CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

```

1 COMPUTER READABLE FORM:
2
3 MEDIUM TYPE: Floppy disk
4
5 COMPUTER: IBM PC compatible
6
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8
9 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2.2
10
11 CURRENT APPLICATION F.A.V.A:
12
13 APPLICATION NUMBER: US/60/082,300
14
15 FILING DATE: HEREWITH
16
17 CLASSIFICATION:
18
19 ATTORNEY/AGENT INFORMATION:
20
21 NAME: GERROLD, MICHAEL C.
22
23 REGISTRATION NUMBER: 39,132
24
25 REFERENCE/DOCKET NUMBER: PM-00014 P
26
27 TELECOMMUNICATION INFORMATION:
28
29 TELEPHONE: (650) 855-0555
30
31 TELEFAX: (650) 845-4166
32
33 INFORMATION FOR SRQ ID NO: 11599:
34
35 SEQUENCE CHARACTERISTICS:
36
37 LENGTH: 7997 base pairs
38
39 TYPE: nucleic acid
40
41 STRANDEDNESS: double

```

TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLONE: AFU1c11615
us-60-082-300-11599

Query Match 76.7%; Score 279.8; DB 47; Length 7997;
Best Local Similarity 92.1%; Pred. No. 2,7e-62;
Matches 339; Conservative 0; Mismatches 22; Indels 6; Gaps 4;

OY 1 aaacttcaacaatgcatctctgtgtccggcatcgatgaagaacgacgcaactgcat 60
DB 3933 AAACCTTCACACGCGATCTTGTTCCGGCATCGATGAGAAAGCGACGAATGCCAT 3992
OY 61 aagtaatgtaattgcagaatlcagtaacatcagagtccttgaaacgacatgcccc 120
DB 3993 AAGTAATGTGAATTGCAGAAATTCAGTGAATCATGAGACTTTGAACGACACATTCGCGCCC 4052
OY 121 ccggatccgggggggagctgtccgaagcgtatgctccctcaagcccgctgtg 180
DB 4053 CTGGATTCTCGGGGGGCGATGCTGTCCAGCGTCATTCCTCCCTCAAGCAGCGCTGTG 4112
OY 181 tcttgatcgtcgtccccc-cccccgggggagcggccccgaagaacgacgagccg-9 238
DB 4113 TGTTGGGCCCGCGTCCCTCTCCCGGGGAGCGGCCGGAAGGACGCGGCGACCGCG 4172
OY 239 tccggtcctcgaagcgtatgaggcttgtaaccgcgtcgaatgaaggccggcgccag 298
DB 4173 TCCTGCTCTCAGCGCTATGGGGCTTTGTCACCTGCTC--TGTAGCCCGCGCGCGCAG 4230
OY 299 ccgggtcctcgaactcttcttcaggtgacgtgcgagtaggagtagacgctg 358
DB 4231 CCGAC--ACCCAACTTATTTTCTAAGGTTGACCTCGATCAGTAGGATACCGCTG 4288
OY 359 aacttaa 365
DB 4289 AACTTAA 4295

RESULT 15
US-09-580-797-35
Sequence 35, Application US/09580797
GENERAL INFORMATION:
APPLICANT: Iwen, Peter C.
APPLICANT: Hinrichs, Steven H.
APPLICANT: Henry, Travis
APPLICANT: Board of Regents of the University of Nebraska
TITLE OF INVENTION: Materials and Methods for Molecular
TITLE OF INVENTION: Detection of Clinically Relevant Pathogenic Fungal Species
FILE REFERENCE: UNMC 63149
CURRENT APPLICATION NUMBER: US/09/580,797
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 597
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-09-580-797-35

Query Match 76.2%; Score 278.2; DB 22; Length 597;
Best Local Similarity 92.1%; Pred. No. 4.6e-62;
Matches 338; Conservative 0; Mismatches 23; Indels 6; Gaps 4;

OY 1 aaacttcaacaatgcatctctgtgtccggcatcgatgaagaacgacgcaactgcat 60
DB 215 aaacttcaacaacgagctccttggtccggcatcgatgaagaacgacgcaaatgcat 274
OY 61 aagtaatgtaattgcagaatlcagtaacatcagagtccttgaaacgacatgcccc 120
DB 275 aactaatgtaattgcagaatlcagtaacatcagagtccttgaaacgacatgcccc 334

OY 121 ctggcatccgggggggcatgctgtccgaagcgtatgctgtccctaaagccggtctg 180
DB 335 ctggtatccgggggggcatgctgtccgaagcgtatgctgtccctaaagcaggtctg 394
OY 181 tcttgatcgtcgtccccc-cccccgggggagcggccccgaagaacgacgagccgacacg-9 238
DB 395 tcttgagcccccgtcccccctcccggggagcggccccgaagaacgacgagccgacacg 454
OY 239 tccggtcctcgaagcgtatgaggcttgtaaccgcgtcgaatgaaggccggcgccag 298
DB 455 tccggtcctcgaagcgtatgaggcttgtaaccgcgtc--tgtagcccgcgccgacag 512
OY 299 ccgggtcctcgaactcttcttcaggtgacgtgcgagtaggagtagacccgctg 358
DB 513 ccgac--accgaacttatttcttaagtgaccccgatcagtaggagtagacccgctg 570
OY 359 aacttaa 365
DB 571 aacttaa 577

Search completed: August 22, 2002, 00:39:26
Job time: 13051 sec

|

.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:40 ; Search time 663.62 Seconds
(without alignments)
1479.886 Million cell updates/sec

Title: US-10-046-955-5

Perfect score: 365

Sequence: 1 aaacttcaacaatgacatc.....gggatacccgctgaactaa 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1721111 seqs, 1345317543 residues

3442222

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA, New: *
1: /cgn2_6/p/oddata/2/pna/US06_NEW_COMB.seq:*
2: /cgn2_6/p/oddata/2/pna/US07_NEW_COMB.seq:*
3: /cgn2_6/p/oddata/2/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/p/oddata/2/pna/US09_NEW_COMB.seq:*
5: /cgn2_6/p/oddata/2/pna/US10_NEW_COMB.seq:*
6: /cgn2_6/p/oddata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/p/oddata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/p/oddata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	365	100.0	365	7	US-10-046-955-5
2	284.2	77.9	365	7	US-10-046-955-3
3	258.8	70.9	364	7	US-10-046-955-2
4	230.4	63.1	355	7	US-10-046-955-4
5	206.6	56.6	309	7	US-10-046-955-28
6	189.4	51.9	641	5	US-09-766-173C-4
7	184	50.4	618	5	US-09-766-173C-5
8	169	46.3	532	1	PCT-US02-11769-2
9	162.6	44.5	536	5	US-09-517-790-5
10	159	43.6	650	1	PCT-US02-11769-4
11	153.8	42.1	515	5	US-09-517-790-1
12	153.8	42.1	523	5	US-09-517-790-4
13	143.2	39.2	516	5	US-09-517-790-2
14	143.2	39.2	570	5	US-09-517-790-3
15	123.2	33.8	310	7	US-10-046-955-7
16	123.2	33.8	319	7	US-10-046-955-6
17	107.6	29.5	208	7	US-10-046-955-1
18	101.6	27.8	336	7	US-10-046-955-29
19	95.4	26.1	346	7	US-10-046-955-26
20	94.8	25.9	346	7	US-10-046-955-25
21	94.4	25.9	343	7	US-10-046-955-27
22	90	24.7	1414	7	US-10-155-881-6537
23	88.8	24.3	1351	7	US-10-155-881-6113
24	87.6	24.0	250	5	US-09-975-254-4536
25	87	23.8	2091	5	US-09-935-625-5545

C	26	87	23.8	2091	5	US-09-935-625-17457	Sequence 17457, A
C	27	87	23.8	2091	5	US-09-935-625-25792	Sequence 25792, A
C	28	87	23.8	2097	5	US-09-935-625-5599	Sequence 5599, Ap
C	29	87	23.8	2097	5	US-09-935-625-6116	Sequence 6116, Ap
C	30	87	23.8	2097	5	US-09-935-625-17511	Sequence 17511, A
C	31	87	23.8	2097	5	US-09-935-625-18547	Sequence 18547, A
C	32	87	23.8	2097	5	US-09-935-625-25913	Sequence 25913, A
C	33	87	23.8	2097	5	US-09-935-625-26950	Sequence 26950, A
C	34	87	23.8	4310	7	US-10-177-253-71	Sequence 71, Appl
C	35	84.8	23.2	1474	7	US-10-155-881-2900	Sequence 2900, Ap
C	36	84.4	23.1	511	5	US-09-975-254-5041	Sequence 5041, Ap
C	37	84.2	23.1	131	7	US-10-155-881-1757	Sequence 1757, Ap
C	38	83.4	22.8	835	7	US-10-155-881-4283	Sequence 4283, Ap
C	39	83.4	22.8	949	7	US-10-155-881-3328	Sequence 3328, Ap
C	40	83.4	22.8	1037	7	US-10-155-881-2313	Sequence 2313, Ap
C	41	83.4	22.8	1180	7	US-10-155-881-2120	Sequence 2120, Ap
C	42	83.4	22.8	1545	7	US-10-155-881-226	Sequence 226, App
C	43	83.4	22.8	3480	8	US-60-391-781-202	Sequence 202, App
C	44	81.8	22.4	1015	7	US-10-155-881-2286	Sequence 2286, Ap
C	45	81.8	22.4	1226	8	US-60-391-781-664	Sequence 664, App

ALIGNMENTS

RESULT 1
US-10-046-955-5
Sequence 5, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorovich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 365
TYPE: DNA
ORGANISM: Aspergillus nidulans
US-10-046-955-5

Query Match 100.0%; Score 365; DB 7; Length 365;

Best Local Similarity 100.0%; Pred. No. 2.8e-90;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	aaacttcaacaatgacatcctctggtccggcatcgatgaagaacgacgacatcgat	60
DB	1	aaacttcaacaatgacatcctctggtccggcatcgatgaagaacgacgacatcgat	60
QY	61	aagtaatgtaattgcgaattcagtaacatcgatgctcttgaacgacatcgacccc	120
DB	61	aagtaatgtaattgcgaattcagtaacatcgatgctcttgaacgacatcgacccc	120
QY	121	ctggcatccgggggagatcgctcgcagacgcatgctgctcctcaagccgctgtg	180
DB	121	ctggcatccgggggagatcgctcgcagacgcatgctgctcctcaagccgctgtg	180
QY	181	tgttggtcgtcgtcccccgggggagcgggcccgaaggaagcagcgcgacccgtc	240

QY	1	aacttccaacatgatactctctgtgtlccggatcagatgaagaacgacgaaactgcgat	60
Db	1	aaacttccaacatgatactctctgtgtlccggatcagatgaagaacgacgaaactgcgat	60
QY	61	aagtaatgtaattgagagaattcagtgatcatcgaattctttgaagacacattggcccc	120
Db	61	aactaagtgtaattgagagaattcagtgatcatcgaattctttgaagacacattggcccc	120
QY	121	ctggacattccgggggggacatgcgtctcagcagcagtcattgcctgcgcc - tcaagcccgagcttgt	179
Db	121	ctggatattccgggggggacatgcgtctcagcagcagtcattgcctgcgcc - tcaagcccgagcttgt	180
QY	180	gtgtttgtgtctgcgtccccc - ccccccgggggaacgggcgcgaaagcagcgcgcgcgcg -	237
Db	181	gtgtttgtgtgtcccccctcccccctcccccgggggaacgggcgcgaaagcagcgcgcgcgcg -	240
QY	238	gtccggtctctcagcagcgtatagggctcttggtaccccgcgtcagatgaagccgcgcgcgcgcga	297
Db	241	gtccggtctctcagcagcgtatagggctctg - - - tcaactgcgtctgttaagccgcgcgcgcgcga	297
QY	298	ggcggcgctctccaacctatcttctccaaagttgcacctgcagatcagtgagatataccgct	357
Db	298	ggcggac - acccaacttatatttctctaagtgatgcacctgcagtgagatataccgct	355
QY	358	gaactctaa	365
Db	356	gaactctaa	363


```
; Sequence 4, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Aspergillus terreus
US-10-046-955-4

Query Match          63.1%; Score 230.4; DB 7; Length 355;
Best Local Similarity 87.6%; Pred. No. 1,7e-53;
Matches 312; Conservative 0; Mismatches 31; Indels 13; Gaps 5;

OY 1 aaattcaacaatgatactcttggttcggagcatcgatgaagaacgacgactcgat 60
    |||||
DB 1 aaattcaacaatgatactcttggttcggagcatcgatgaagaacgacgactcgat 60
    |||||

OY 61 aagtaatgataatgataatgataatgataatgataatgataatgataatgata 120
    |||||
DB 61 aactaatgataatgataatgataatgataatgataatgataatgataatgata 120
    |||||

OY 121 ctgagatccgag-gggacatgctgtccgagcgtcaatgtctgacctcaagccgctgt 179
    |||||
DB 121 ctgagatccgagggggagcatgctgtccgagcgtcaatgtctgacctcaagccgctgt 180
    |||||

OY 180 ggttgaggtcgtgctccccc-----ccccgggggagcgccgaaagcgagcgcgacgc 237
    |||||
DB 181 ggttgaggtcgtgctcccccggctcccgaggacgggcccgaagcgagcgcgacgc 240
    |||||

OY 238 -gtccggctcccgagcatgaggtgtgtaccccgctcgattagggcgcgcgcgcc 296
    |||||
DB 241 cgtccggctcccgagcatgaggtgtgtaccccgctcgattagggcgcgcgcgcc 299
    |||||

OY 297 agccggcgctccca-----acctatcttctcaggttgaacctcgatcagat 344
    |||||
DB 300 gccgagcagcatatttgcgaactggtttttttccaggttgcacctcgatcagat 355
    |||||

RESULT 5
US-10-046-955-28
; Sequence 28, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morrison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
```

```
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Penicillium notatum
US-10-046-955-28

Query Match          56.6%; Score 206.6; DB 7; Length 309;
Best Local Similarity 87.0%; Pred. No. 5.4e-47;
Matches 274; Conservative 0; Mismatches 34; Indels 7; Gaps 4;

OY 52 aactcgataatgataatgataatgataatgataatgataatgataatgataatg 111
    |||||
DB 1 aactcgataatgataatgataatgataatgataatgataatgataatgataatg 59
    |||||

OY 112 ttgcgccccctggatccgggggagcatgctgtccgagcgtcaatgtctgacctcaagcc 171
    |||||
DB 60 ttgcgccccctggatccgggggagcatgctgtccgagcgtcaatgtctgacctcaagca 119
    |||||

OY 172 cggctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 231
    |||||
DB 120 cggctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 179
    |||||

OY 232 gacccg-gtccggctctcgagcgtatgaggtgtgtgtgtgtgtgtgtgtgtgtgt 290
    |||||
DB 180 gacccggtctcgagcgtatgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 237
    |||||

OY 291 ggcgcaagccggcgtctcaaccttattcttcaggttgaacctcgagcaggtagggat 350
    |||||
DB 238 ggcgcttgcgagcaaccacaattt---ttatcaggttgaacctcgagcaggtagggat 294
    |||||

OY 351 acccgctgaactaa 365
    |||||
DB 295 acccgctgaactaa 309
    |||||

RESULT 6
US-09-766-173C-4
; Sequence 4, Application US/09766173C
; GENERAL INFORMATION:
; APPLICANT: Carroll, George C.
; TITLE OF INVENTION: Materials and Methods For Detection of
; FILE REFERENCE: Oregon 99-09
; CURRENT APPLICATION NUMBER: US/09/766,173C
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/01735
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/177,013
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Gulignardia Citricarpa
US-09-766-173C-4

Query Match          51.9%; Score 189.4; DB 5; Length 641;
Best Local Similarity 73.7%; Pred. No. 3.1e-42;
Matches 272; Conservative 0; Mismatches 86; Indels 11; Gaps 2;

OY 1 aaattcaacaatgatactcttggttcggagcatcgatgaagaacgacgactcgat 60
```

```
Db 267 aaacttcaacaacgatctctgttctgcgcacgtatgaagaacgcagcaatgcgat 326
Qy 61 aagtaatggaattgcaagatcagtgaaatcagatgcgtttgaaacgaatctgcccc 120
Db 327 aagtaatggaattgcaagatcagtgaaatcagatgcgtttgaaacgaatctgcccc 386
Qy 121 ctggcattccgggggcaagcctgtccagagctcattgtcgtccctcaagcccgctgtg 180
Db 387 ctggcattccgggggcaagcctgtctgcagcgtcattcaaccctcaagcctctgtgtg 446
Qy 181 tgttggtcgtcgtcccccggggggaagcgccgaagcaagcgagcgacgcgtc 240
Db 447 atctg-----gcagacgtccgtccggagcgctgtgaaagacctcgagcgagcgtct 499
Qy 241 cggctccgagcgataggggctgtgacccgcctgattgaagcgccggcgagcgag-- 298
Db 500 cggctccgagcgatagaaataatctgccttggaagaggggagcgctgtgcgcgcga 559
Qy 299 --cggcgctcccaactatcttctcaggttgacctcgatcagtagagataccgcg 356
Db 560 caatcgacctgcgtcacatatttccaaggttgacctcgatcagtagagataccgcg 619
Qy 357 tgaactaa 365
Db 620 tgaactaa 628
```

RESULT 7
US-09-766-173C-5

```
; Sequence 5, Application US/09766173C
; GENERAL INFORMATION:
; APPLICANT: Carrol, George C.
; TITLE OF INVENTION: Materials and Methods For Detection of
; TITLE OF INVENTION: Pathogenic Guinardia Citricarpa
; FILE REFERENCE: Oregon 99-09
; CURRENT APPLICATION NUMBER: US/09/766,173C
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/01735
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/177,013
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Guinardia Citricarpa
US-09-766-173C-5
```

Query Match 50.4%; Score 184; DB 5; Length 618;
Best Local Similarity 73.1%; Pred. No. 9.2e-41;
Matches 266; Conservative 0; Mismatches 90; Indels 8; Gaps 2;

```
Qy 1 aaacttcaacaatgatactctgttccggcagatcgaagaacgcagcaatgcgat 60
Db 262 aaacttcaacaacgatctctgttctgcgcacgtatgaagaacgcagcaatgcgat 321
Qy 61 aagtaatggaattgcaagatcagtgaaatcagatgcgtttgaaacgaatctgcccc 120
Db 322 aagtaatggaattgcaagatcagtgaaatcagatgcgtttgaaacgaatctgcccc 381
Qy 121 ctggcattccgggggcaagcctgtccagagctcattgtcgtccctcaagcccgctgtg 180
Db 382 ctggcattccgggggcaagcctgtctgcagcgtcattcaaccctcaagcctctgtgtg 441
Qy 181 tgttggtcgtcgtcccccggggggaagcgccgaagcaagcgagcgacgcgtc 240
Db 442 atctg-----gcagacgtccgtccggagcgctgtgaaagacctcgagcgagcgtcc 494
Qy 241 cggctccgagcgataggggctgtgacccgcctgattgaagcgccggcgagcgag--c 299
```

```
Db 495 tagctcgagctagtagtaaaatatactcgtttgaggtgtctgagcgagcgccgcgac 554
Qy 300 cggcgtcccaacttatcttctcaggttgacctgagatcgaagtaggataccgctga 359
Db 555 aatcgacctgtctatttccaaagttgacctcgatcgaagtaggataccgctga 614
Qy 360 actt 363
Db 615 actt 618
```

```
RESULT 8  
PCT-US02-11769-2  
; Sequence 2, Application PC/TUS0211769  
; GENERAL INFORMATION:  
; APPLICANT: Strobel, Gary  
; APPLICANT: Menker, Denise  
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF  
; TITLE OF INVENTION: USE  
; FILE REFERENCE: AQ 2019, 40  
; CURRENT APPLICATION NUMBER: PCT/US02/11769  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/283,902  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: 60/363,072  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 652  
; TYPE: DNA  
; ORGANISM: Muscodor albus  
PCT-US02-11769-2
```

Query Match 46.3%; Score 169; DB 1; Length 652;
Best Local Similarity 70.7%; Pred. No. 1.2e-36;
Matches 258; Conservative 0; Mismatches 95; Indels 12; Gaps 2;

```
Qy 1 aaacttcaacaatgatactctgttccggcagatcgaagaacgcagcaatgcgat 60
Db 278 aaacttcaacaacgatctctgttctgcgcacgtatgaagaacgcagcaatgcgat 337
Qy 61 aagtaatggaattgcaagatcagtgaaatcagatgcgtttgaaacgaatctgcccc 120
Db 338 aagtaatggaattgcaagatcagtgaaatcagatgcgtttgaaacgaatctgcccc 397
Qy 121 ctggcattccgggggcaagcctgtccagagctcattgtcgtccctcaagcccgctgtg 180
Db 398 ttagcattctagttggtcgttctgcagcgtcattcaaccctcaagcctgtgtgt 457
Qy 181 tgttggtcgtcgtcccccggggggaagcgccgaagcaagcgagcgacgcgtc 240
Db 458 ag--cgttggaagcctcagcagcagcgtcagctcctcaagagtgatgtggaggtgtg 515
Qy 241 cggctccgagcgataggggctgtgacccgcctgattgaagcgccggcgagcagcc 300
Db 516 ctcaacttagcgagtagtaaatctatctcgcctctgtagttgttccggc-----cc 565
Qy 301 ggcgtcccaacttatcttctcaggttgacctggaatcagtaggataccgctga 360
Db 566 ctgcgtaaaacccctatatacaaggttgacctcgatcagtaggataccgctga 625
Qy 361 cttaa 365
Db 626 cttaa 630
```

RESULT 9
US-09-517-790-5
; Sequence 5, Application US/09517790
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F

```

1  TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of Ru
2
3  TITLE OF INVENTION: Diseases in Plants
4  FILE REFERENCE: RU-0093
5
6  CURRENT APPLICATION NUMBER: US/09/517,790
7
8  CURRENT FILING DATE: 2000-03-02
9
10 PRIOR APPLICATION NUMBER: US 60/123,099
11
12 PRIOR FILING DATE: 1999-03-05
13
14 NUMBER OF SEQ ID NOS: 5
15
16 SOFTWARE: PatentIn version 3.1
17
18 SEQ ID NO 5
19
20 LENGTH: 536
21
22 TYPE: DNA
23
24 ORGANISM: Ampelomyces humuli
25
26 US-09-517-790-5

```

Query Match	44.58;	Score 162.6;	DB 5;	Length 536;
Best Local Similarly	71.58;	Pred. No. 6.3e-35;		
Matches 261; Conservative	0;	Mismatches 89;	Indels 15;	Gaps 3;

QY	2	aactttcaacatgcatctcttggtcttcgcgcacatcgatggaagacgcgcgaacttcgcata	61
Db	170	aactttcaacaaacgcatctctcttggtcttcgcacatcgatggaagacgcgcgaacttcgcata	229
OY	62	agtaatcgaaatctcagaatctcaatcgataatcgcagcttccttgaaacgcacatctgcgcgcc	121
Db	220	agtcgtctggaattctgcagaatttcgaatcgatgataatcgaactcttgaaacgcacatttgcgcgcc	289
OY	122	tcgcacatccgggggggcabtcgcctctgcagcgagcgctcaatctgccttcgacacgccgcgccttggt	181
Db	290	tcgattctccatcgvggcacatgcctctcttcgagcgctcaatttgtaacttcacaaagcctctcttg-gt	348
OY	182	gttcggtcgtctgcgtcccccgcgcgcgcgggagacgcgcgcgaagaagcgcgcgacacgcgtcc	241
Db	349	gttcgggtgtcttgctcgcgcctctcgtcgtta-----gacttcgcctcaaaaacat	395
OY	242	ggtccctcgacgctatgvggcctctgtctcacccgcctcgatctagcgccgcgcgcgcgcga-gcc	300
Db	396	tcgcacgacccggcggtatctgcaatttcgcagagacgataatctgcgccttgcactatcatalaagac	455
OY	301	ggcgctcccaaaccttatctcttcacagttcgacactcgatcgaatcgaatgaagatccgcgtgaa	360
Db	456	gacgcacaaagaatcactttttacaactcttcgacccctcgatcgaatcgaatgaagatcaccgcgtgaa	515
OY	361	cttaa 365	
Db	516	cttaa 520	

```

RESULT 10
PCT-US02-11769-4
: Sequence 4 Application PC/TUS0211769
:
: GENERAL INFORMATION:
: APPLICANT: Strödel, Gary
: APPLICANT: Marker, Denise
: TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
: TITLE OF INVENTION: USE
: FILE REFERENCE: AQ 2019, 40
: CURRENT APPLICATION NUMBER: PCT/US02/11769
: CURRENT FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 60/283, 902
: PRIOR FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: 60/363, 072
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
:
: LENGTH: 650
:
: TYPE: DNA
:
: ORGANISM: Muscador roseus
PCT-US02-11769-4

```

Query Match	43.6%	Score 159;	DB 1;	Length 650;
Best Local Similarity	69.0%	Pred. No. 6.3e-34;		
Matches 252; Conservative	0;	Mismatches 100;	Indels 13;	Gaps 2

2

[illegible]

```

RESULT 11
US-09-517-790-1
; Sequence 1, Application US/09517790
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F
; TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of
; TITLE OF INVENTION: Diseases in Plants
; FILE REFERENCE: RU-0093
; CURRENT APPLICATION NUMBER: US/09/517,790
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/123,099
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Phoma glomerata
US-09-517-790-1

```

	Query Match	Similarity	88.6%	Score 153.8	Pred. No. 1.6e-32	DB 5	Length 515	
	Best Local	Matches 178	Conservative	0	Mismatches 22	Indels 1	Gaps 1	
Oy	2	aacttcaacaagaatgctctcttggtccgcgcgatgaagaacgcagcgaactgcgata	61					
Dd	187	aacttcaacaagaatgctctcttggtccgcgcgatgaagaacgcagcgaatggcata	246					
Oy	62	agtaaatgtgaattgcaggaattcaagtgaalcatcgtagtctttgaacgcacattgcgccccc	121					
Dd	247	agtaagtgtgaattgcaggaattcaagtgaalcatcgtagtctttgaacgcacattgcgccccc	306					
Oy	122	tggcattccggaggagatgcgttcgcagagcatattgctgcacctaaagccccgttgt	181					
Dd	307	tgttatcccatggggcagtcgctgttcgagcgccaattgtacccttcaaagccttcgttg-gt	365					
Oy	182	gttcgggtcgctgcgtccccc	202					
Dd	366	gttcgggtcgctgcgtccccc	386					

```

RESULT 12
US-09-517-790-4
: Sequence 4, Application US/09517790
:
: GENERAL INFORMATION:
: APPLICANT: White, Jr., James F
: TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of Fus
: TITLE OF INVENTION: Diseases in Plants
: FILE REFERENCE: RU-0093
: CURRENT APPLICATION NUMBER: US/09/517,790
: CURRENT FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: US 60/123,099
: PRIOR FILING DATE: 1999-03-05
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 523
: TYPE: DNA
: ORGANISM: Phomo glomerata
US-09-517-790-4

```

Query Match	42.18;	Score 153.8;	DB 5;	Length 523;
Best Local Similarity	88.68;	Pred. No. 1.6e-32;		
Matches 178;	Conservative	0;	Mismatches 22;	Indels 1;
			Gaps	1.

[illegible]

```

RESULT 13
US-09-517-790-2
: Sequence 2, Application US/09517790
: GENERAL INFORMATION:
: APPLICANT: White, Jr., James F
: TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of Fy
: TITLE OF INVENTION: Diseases in Plants
: FILE REFERENCE: RU-0093
: CURRENT APPLICATION NUMBER: US/09/517,790
: CURRENT FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: US 60/123,099
: PRIOR FILING DATE: 1999-03-05
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
:
: LENGTH: 516
:
: TYPE: DNA
: ORGANISM: Amelomyces quisqualis
US-09-517-790-2

```

Query Match:	39.2%	Score 143.2:	DB 5,	Length 516;
Best Local Similarity:	Pred. 10.1:	3e-29;		
Matches 183;	Conservative 0;	Mismatches 48;	Indels 1;	Gaps 1.

Oy	2	aacttcaacatgatcctcttggttcgcgcacatgaagaacgcagcaactgcgata	61
db	202	aacttcaacacacagctcctcttggttcgcgcacatgaagaacgcagcaactgcgata	261

[illegible]

```

: RESULT 14
: US-09-517-790-3
: Sequence 3, Application US/09517790
: GENERAL INFORMATION:
: APPLICANT: White, Jr., James F
: TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of
: TITLE OF INVENTION: Diseases in Plants
: FILE REFERENCE: RU-0093
: CURRENT APPLICATION NUMBER: US/09/517,790
: CURRENT FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: US 60/123,099
: PRIOR FILING DATE: 1999-03-05
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 570
: TYPE: DNA
: ORGANISM: Ampeelomyces quisqualis
: US-09-517-790-3

```

Query Match	39.28;	Score 143.2;	DB 5;	Length 570;
Best Local Similarity	78.98;	Pred. No. 1.3e-29;		
Matches 183; Conservative	0;	Mismatches 48;	Indels 1;	Gaps 1;

[illegible]

RESULT 15
 US-10-046-955-7
 : Sequence 7, Application US/10046955
 : GENERAL INFORMATION:
 : APPLICANT: The Government of the United States of America, as Represented by the
 : APPLICANT: Secretary of the Department of Health and Human Services, Centers for
 : APPLICANT: Control and Prevention
 : APPLICANT: Morrison, Christine J.
 : APPLICANT: Reiss, Errol
 : APPLICANT: Aidorevich, Lilliana
 : APPLICANT: Choi, Jong Soo
 : TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
 : TITLE OF INVENTION: Other Filamentous Fungi
 : FILE REFERENCE: 6395-62064
 : CURRENT APPLICATION NUMBER: US/10/046,955
 : CURRENT FILING DATE: 2002-06-04
 : PRIOR APPLICATION NUMBER: US 09/423,233
 : PRIOR FILING DATE: 2000-06-27

;; PRIOR APPLICATION NUMBER: PCT/US98/08926
;; PRIOR FILING DATE: 1998-05-01
;; PRIOR APPLICATION NUMBER: US 60/045,400
;; PRIOR FILING DATE: 1997-05-02
;; NUMBER OF SEQ ID NOS: 61
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 7
;; LENGTH: 310
;; TYPE: DNA
;; ORGANISM: Fusarium moniliforme
US-10-046-955-7

Query Match 33.8%; Score 123.2; DB 7; Length 310;
Best Local Similarity 66.5%; Pred. No. 3.4e-24;
Matches 210; Conservative 0; Mismatches 98; Indels 8; Gaps 2;

QY 52 aactgcataatgaatgtgaatcagagaatcagaatcagagccttgaagcaca 111
DB 1 aatgcataatgaatgtgaatcagagaatcagaatcagagccttgaagcaca 60
QY 112 ttgcgccccctggcattccgggggagcatgctgcgagcgcatgtgcccctaag-- 169
DB 61 ttgcgcccccgagatctctggcgagcatgctgcgagcgcatgttccaacctcaagcc 120
QY 170 ccgagctgtgtgttggtgctgcgtcccccgggggagcgcccgaaagcagcgg 229
DB 121 ccgagctgtgtgttggtgagcagcgcccttgcgcaagcgcccgaaatctagt 180
QY 230 cggcacccggtcgcgtcctcagcgctatgaggctgtgcacccgctcgattagggcgcc 289
DB 181 gcggtcgcgtcagcgtccatctgctagtagtaaaacctgc-----aactgtacg 234
QY 290 gggcgccagccggcgtctccaaccttacttctcaggtgacctcgatcaggtagga 349
DB 235 cggcgcgccagccagcgttaaaaccccccaactctgaatgtgacctcgatcaggtagga 294
QY 350 taaccgctgaactaa 365
DB 295 taaccgctgaactaa 310

Search completed: August 22, 2002, 00:50:48
Job time: 1188 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:44 : Search time 2238.68 Seconds
(Without alignments)
2981.920 Million cell updates/sec

Title: US-10-046-955-6
Perfect score: 319
Sequence: 1 gaaatgcataaataatgt.....ggaatacccgctgaacttaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_com:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_inv:*
33: em_higo_inv:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

1	319	100.0	319	8	AF117921	AF117921 Nectria h
2	308	96.6	509	8	AF165874	AF165874 Nectria h
3	298.6	93.6	550	8	AF178394	AF178394 Nectria h
4	298.6	93.6	550	8	AF178401	AF178401 Nectria h
5	298.6	93.6	569	8	AF129104	AF129104 Nectria h
6	297	93.1	548	8	AF178397	AF178397 Fusarium
7	294.6	92.4	549	8	AF178398	AF178398 Nectria l
8	288.6	90.5	548	8	AF178413	AF178413 Neocosmos
9	288.2	90.3	548	8	AF178402	AF178402 Fusarium
10	287	90.0	547	8	AF178412	AF178412 Neocosmos
11	285.6	89.5	544	8	NEKITS	L36627 Neocosmospo
12	280.2	87.8	550	8	AF178406	AF178406 Fusarium
13	279	87.5	480	8	AF150466	AF150466 Nectria h
14	279	87.5	480	8	AF150467	AF150467 Nectria h
15	279	87.5	480	8	AF440567	AF440567 Nectria h
16	277.2	86.9	550	8	AF178422	AF178422 Fusarium
17	276.2	86.6	552	8	AF178411	AF178411 Nectria h
18	275.6	86.4	550	8	AF178407	AF178407 Fusarium
19	275.6	86.4	550	8	AF178408	AF178408 Fusarium
20	275	86.2	547	8	NECITSA	L36619 Nectria hae
21	270.6	84.8	549	8	AF178409	AF178409 Fusarium
22	269.2	84.4	548	8	AF178416	AF178416 Nectria h
23	268	84.0	548	8	AF178395	AF178395 Nectria h
24	268	84.0	548	8	AF178404	AF178404 Fusarium
25	268	84.0	566	8	AF130142	AF130142 Nectria h
26	267.4	83.8	518	8	AF437761	AF437761 Fungal ls
27	265.8	83.3	547	8	AF178410	AF178410 Nectria h
28	265	83.1	545	8	NECITSR	L36620 Nectria hae
29	265	83.1	552	8	AF178421	AF178421 Nectria h
30	263	82.4	544	8	AF178399	AF178399 Fusarium
31	262.8	82.4	544	8	NECITS	L36616 Nectria hae
32	262.2	82.2	478	8	AF132801	AF132801 Nectria h
33	262.2	82.2	478	8	AF150459	AF150459 Nectria h
34	262.2	82.2	478	8	AF150460	AF150460 Nectria h
35	262.2	82.2	478	8	AF150461	AF150461 Nectria h
36	262.2	82.2	478	8	AF150462	AF150462 Nectria h
37	262.2	82.2	478	8	AF150463	AF150463 Nectria h
38	262.2	82.2	478	8	AF150464	AF150464 Nectria h
39	261.8	82.1	593	8	NH094684	U94684 Nectria hae
40	261.4	81.9	479	8	AF150475	AF150475 Nectria h
41	261.2	81.9	550	8	AF178400	AF178400 Fusarium
42	261.2	81.9	553	8	AF178403	AF178403 Fusarium
43	261.2	81.9	568	8	AF130140	AF130140 Nectria h
44	261.2	81.9	1178	8	FSOITSRGNA	L36630 Fusarium so
45	261.2	81.9	1178	8	FSOITSRGNB	L36632 Fusarium so

ALIGNMENTS

RESULT 1

AF117921 319 bp DNA linear PLIN 17-JUN-2000

LOCUS

DEFINITION Nectria haematococca 5.8S ribosomal RNA gene, partial sequence; Internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF117921

VERSION AF117921.1 GI:8570107

KEYWORDS

SOURCE Nectria haematococca.

ORGANISM Nectria haematococca

REFERENCE 1 (bases 1 to 319)

REFERENCE 2 (bases 1 to 319)

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REFERENCE 414 (bases 1 to 319)

REFERENCE 415 (bases

FEATURES
source
1. .319
/db_xref="Nectria haematococca"
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1. .159
misc_RNA
/product="5.8S ribosomal RNA"
160. .272
/note="ITS2"
/product="Internal transcribed spacer 2"
273. .>319
/product="28S ribosomal RNA"
BASE COUNT 77 a 96 c 84 g 62 t
ORIGIN

Query Match 100.0%; Score 319; DB 8; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.1e-77;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaaatgcgataagtaatgtaattgcaagaattcagtcgaatcatcgaatccttgaagca 60
|||||
Db 1 GAAATGCATAGTAATGTAATGCAAGATTCACTGATCATGGAATCTTGAACGCA 60
|||||
OY 61 catgcccgcgcagatctctggcggagatgcctgttcgaagcgaattacaacctcagg 120
|||||
Db 61 CATTCGCGCCGCGCAGATTCTGGCGGCGATGCTTTCAGCGCTCATTTACAACCTCAGG 120
|||||
OY 121 ccccgagcctgagcgttggggaatcggagaaagcccccctgcggagcaaacgcccgtcccca 180
|||||
Db 121 CCCCCGGCCTGGCTTGGGGATCGCGGAGCCCTTCGGGACACAGCGCTCCCA 180
|||||
OY 181 aatcacgtagcgttccgcgcgaagcttcattgctgaagtagtaaacctcgaactgga 240
|||||
Db 181 AATACAGTGGCGGTCCCGCGCAGCTTCATTGCGTAGAGTAACACTCGCAACTGGA 240
|||||
OY 241 gagcggcgagcgcagcgcgttaaaacccaacttcgaatgttgacccctgaatcaggtag 300
|||||
Db 241 GAGCGCGGCGGCGCCGCTTAACACCCACTTGTGAATGTTGAAATCGAATCAGGTAG 300
|||||
OY 301 gaataccgcgtgaactaa 319
|||||
Db 301 GAATACCGCTGAACCTTA 319

RESULT 2
AF165874
LOCUS AF165874 509 bp DNA linear PLN 18-JUL-1999
DEFINITION Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF165874
VERSION AF165874.1 GI:5524731
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 509)
Iwen,P.C., Henry,T. and Hinrichs,S.H.
Sequence analysis of the internal transcribed spacer regions of Fusarium species most commonly associated with human invasive disease
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 509)
Iwen,P.C., Henry,T. and Hinrichs,S.H.
Direct Submission
JOURNAL Submitted (07-JUL-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6495, USA
FEATURES
source Location/Qualifiers
1. .509
/organism="Nectria haematococca"
/strain="ATCC2877"

misc_RNA
/db_xref="ATCC:62877"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
1. .150
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/note="ITS1"
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151. .307
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308. .480
/note="ITS2"
/product="Internal transcribed spacer 2"
481. .>509
/product="28S ribosomal RNA"
BASE COUNT 130 a 154 c 122 g 103 t
ORIGIN

Query Match 96.6%; Score 308; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.3e-74;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 aatgcgataagtaatgtaattgcaagaattcagtcgaatcatcgaatccttgaagcaca 62
|||||
Db 202 AAATGCGATTAAGTAATGTAATGCAAGATTCACTGATCATGGAATCTTGAACGCA 261
|||||
OY 63 ttgcgcccgcagatctctggcggagatgcctgttcgaagcgaattacaacctcaggcc 122
|||||
Db 262 TTGCGCCGCGCAGATTCTGGCGGCGATGCTTTCAGCGCTCATTTACAACCTCAGGCG 321
|||||
OY 123 cccggagcctgagcgttggggaatcggagaaagcccccctgcggagcaaacgcccgtcccca 182
|||||
Db 322 CCGCGGCTGGCGTGGGGAGATCGCGGAGCCCTTCGGGACACAGCGCTCCCA 181
|||||
OY 183 tacagtgagctccgcgcgaagcttcattgctgaagtagtaaacctcgaactgga 242
|||||
Db 382 TACAGTGGCGGTCCCGCGCAGCTTCATTGCGTAGAGTAACACTCGCAACTGGA 441
|||||
OY 243 gcgcgcgcgcagcgcgttaaaacccaacttcgaatgttgacccctgaatcaggtagga 302
|||||
Db 442 GCGCGGCGGCGCCGCTTAACACCCACTTGTGAATGTTGAAATCGAATCAGGTAGGA 501
|||||
OY 303 ataccgcg 310
|||||
Db 502 ATACCGCG 509

RESULT 3
AF178394
LOCUS AF178394 550 bp DNA linear PLN 20-DEC-2001
DEFINITION Nectria haematococca mpiv strain NRRL22163 18S ribosomal RNA gene, partial sequence; Internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF178394
VERSION AF178394.1 GI:10180235
KEYWORDS
SOURCE Nectria haematococca mpiv.
ORGANISM Nectria haematococca mpiv.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 550)
O'Donnell,K.
Molecular phylogeny of the Fusarium solani species complex
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 550)
O'Donnell,K.
Direct Submission
JOURNAL Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA
FEATURES
source Location/Qualifiers
1. .550
/organism="Nectria haematococca mpiv"
/strain="NRRL22163"

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/db_xref="taxon:135211"
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solani f. sp. xanthoxyli"
<1..>550
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
2, and 28S ribosomal RNA"
BASE COUNT      138 a      158 c      137 g      117 t
ORIGIN

Query Match      93.6%; Score 298.6; DB 8; Length 550;
Best Local Similarity 98.4%; Pred. No. 5.1e-72;
Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY      3 aaatcgataaagtatgtgaattgcgaattcgaatcgaatcgaattcgaagcaca 62
        |||||||
DB      235 AAATCGATAAGTAATGTAATGTCAGAAATTCAGTAATCATCGAATCTTTGAACGACA 294
        |||||||

OY      63 ttggccgccgaagatcttggcgagcgtgctgttcgaacgctcattacaacctcaggcc 122
        |||||||
DB      295 TTGCGCCGCCAGTATGTGGCGGCGATGCTGTTCGACGTCATTACAACTTCAGGCC 354
        |||||||

OY      123 cccgggacctggcgttgggatacgcggaagccccctcgcgacacagccgctcccca 182
        |||||||
DB      355 CCGGGGCTGGCGCTTGGGATCGCGGAGCCGCCCTCGCGGCAC-ACGCCGTCCTTAA 413
        |||||||

OY      183 tacagtggcggtccgcgcgacgtccatctgcgtagtagtaacacacctgcgaactggaga 242
        |||||||
DB      414 TACAGTGGCGGTCCGCCAGCTTCATTGCGTAGTAAACCTCGCAACTGAGAGA 473
        |||||||

OY      243 gcgcgcgccacgcgcgttaaacacccaacttcgaattgtgacctcgatagtagga 302
        |||||||
DB      474 GCGGCGCGCGCACGCCGTAACACCCAACTTCGAAAGTTGACCTCGAATCAGTAGGA 533
        |||||||

OY      303 ataccgcgtgaactaa 319
        |||||||
DB      534 ATACCGCTGAACCTTAA 550
        |||||||

RESULT      4
AF178401      550 bp      DNA      linear      PLN 20-DEC-2001
LOCUS      AF178401
DEFINITION      Nectria haematococca mpiv strain NRRL22277 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION      AF178401
VERSION      AF178401.1 GI:10180242
KEYWORDS
SOURCE      Nectria haematococca mpiv.
ORGANISM      Nectria haematococca mpiv.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE      O'Donnell, K.
AUTHORS      O'Donnell, K.
JOURNAL      Molecular phylogeny of the Fusarium solani species complex
Unpublished
REFERENCE      2 (bases 1 to 550)
AUTHORS      O'Donnell, K.
TITLE      Direct Submission
JOURNAL      Submitted (18-AUG-1999) Microbial Properties Research, NCAR, USDA,
ARS, 1815 N. University St., Peoria, IL 61604, USA
FEATURES
source
1..550
/organism="Nectria haematococca mpiv"
/strain="NRRL22277"
/db_xref="taxon:135211"
/note="forma_specialis: xanthoxyli; anamorph: Fusarium
solani f. sp. xanthoxyli"
<1..>550
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
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BASE COUNT      138 a      158 c      137 g      117 t
ORIGIN

Query Match      93.6%; Score 298.6; DB 8; Length 550;
Best Local Similarity 98.4%; Pred. No. 5.1e-72;
Matches 312; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY      3 aaatcgataaagtatgtgaattgcgaattcgaatcgaatcgaattcgaagcaca 62
        |||||||
DB      235 AAATCGATAAGTAATGTAATGTCAGAAATTCAGTAATCATCGAATCTTTGAACGACA 294
        |||||||

OY      63 ttggccgccgaagatcttggcgagcgtgctgttcgaacgctcattacaacctcaggcc 122
        |||||||
DB      295 TTGCGCCGCCAGTATGTGGCGGCGATGCTGTTCGACGTCATTACAACTTCAGGCC 354
        |||||||

OY      123 cccgggacctggcgttgggatacgcggaagccccctcgcgacacagccgctcccca 182
        |||||||
DB      355 CCGGGGCTGGCGCTTGGGATCGCGGAGCCGCCCTCGCGGCAC-ACGCCGTCCTTAA 413
        |||||||

OY      183 tacagtggcggtccgcgcgacgtccatctgcgtagtagtaacacacctgcgaactggaga 242
        |||||||
DB      414 TACAGTGGCGGTCCGCCAGCTTCATTGCGTAGTAAACCTCGCAACTGAGAGA 473
        |||||||

OY      243 gcgcgcgccacgcgcgttaaacacccaacttcgaattgtgacctcgatagtagga 302
        |||||||
DB      474 GCGGCGCGCGCACGCCGTAACACCCAACTTCGAAAGTTGACCTCGAATCAGTAGGA 533
        |||||||

OY      303 ataccgcgtgaactaa 319
        |||||||
DB      534 ATACCGCTGAACCTTAA 550
        |||||||

RESULT      5
AF129104      569 bp      DNA      linear      PLN 25-MAR-1999
LOCUS      AF129104
DEFINITION      Nectria haematococca 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
transcribed spacer 2, complete sequence; and 28S ribosomal RNA
gene, partial sequence.
ACCESSION      AF129104
VERSION      AF129104.1 GI:4512119
KEYWORDS
SOURCE      Nectria haematococca.
ORGANISM      Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE      Min, B.R.
AUTHORS      Min, B.R.
JOURNAL      Direct Submission
Submitted (17-FEB-1999) Biology, Sangmyung university, 7 Hong Ji
Dong, Chung Ro-gu, Seoul 110-743, Korea
FEATURES
source
1..569
/organism="Nectria haematococca"
/db_xref="taxon:140110"
/note="submitted as Fusarium solani"
<1..30
/product="18S ribosomal RNA"
31..182
/note="ITS-1"
/product="internal transcribed spacer 1"
183..340
/product="5.8S ribosomal RNA"
341..511
/note="ITS-2"
/product="internal transcribed spacer 2"
512..>569
/product="28S ribosomal RNA"
BASE COUNT      151 a      157 c      140 g      121 t
ORIGIN
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QY 63 ttgcgccgcgcagttctctgcgcggcagtccttctcgagcgtcattacaacccctcagcc 122
|||||
Db 293 TTGC GCCGC GCAGTATCTGCGCGGCGCATGCCCTGTTGGAGCGTCATTACACCCCTACGCC 352

QY 123 ccgcggcctgcgttgaggatcgcgcgaagccccctgcgggcacaaagccgtcccca 182

183 tacagtgcggtccgcgcagcttccattgctagtagctaacaacctgcgaactgaga 242

Db 412 TACAGTGGGGTCCCGCCGAGCTTCCATTGCGTAGCTAACACCTCGCAACTGGAGA 471

Db 472 GCGGCGGCGCCACGCCGTAAACACCACTTCTGATGTTGACCTCGAATCAGGTAGCA 531

Db	532	ATACCGCTGA	CTTA	548
27	002	acacccgcgcgaac	ctta	519

RESULT 7
A178308

LOCUS	549 bp	DNA	linear	PLN 20-DEC
DEFINITION	AF178398			
	Nectria ipomoeae strain NRRL22101	185	ribosomal RNA gene, partial	
	sequence: internal transcribed spacer 1	5	95	ribosomal subunit 1

and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

KEYWORDS
Nectria ipomoeae.
SOURCE
ORGANISM
127100001 01.10.100255

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.
1 (bases 1 to 549)

AUTHORS O'Donnell, K.
TITLE Molecular phylogeny of the *Fusarium solani* species complex
JOURNAL Unpublished

AUTHORS
 TITLE
 Journal
 Direct Submission
 O'Donnell, K.
 1993

ARS, 1815 N. University St., Peoria, IL 61604, USA
Location/Qualifiers
1
EAO

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/organism="Nectria ipomoeae"
/strain="NRRL22101"
/db xref="taxon:57162"

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musc_rRNA
<1. .5549
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spa
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BASE COUNT	142 a	158 c	136 g	113 t
ORIGIN	Z, and 203 LIDSONAL NNA			

Query Match	92.48;	Score 294.6;	DB 8;	Length 549;
Best Local Similarity	92.48;	Score 294.6;	DB 8;	Length 549;

Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps

aaatgacgaataaatgttcaaacatttcctggcgcctttccctcccctccccccccc
3

Db 233 AAATGCCATAGTATGTGAATTCGAGATTCAGTGAATCATCGAATCTTTGAACGCACA 292

Db 293 TTGCGCCCGCCAGTATTCGTGCGGGGCATGCTGTTCGAGCGTCATTCAACCCCTGAGGCC 352

OY

123 ccgcggacgtgagcttgygatcgccgaaccgccctgcygcacaacycgtcccccaa 182
|||||
||| ||| |
364 cccccccttcctccctttccatcccccaaaacttaaacatttatataaaaagttaa 197
|||||

QY 63 ttgcgccgcgcagttctctgcgcggcagtccttctcgagcgtcattacaacccctagcc 122

Db 293 ttgcgccgcgcagattctgcgcggcagtccttctcgagcgtcattacaacccctagcc 352

QY 123 ccgcggcctgcgttgaggatcgcgcgaagccccctgcgggcacaaagccgtcccca 182

183 tacagtgcggtccgcgcagcttccattgctagtagctaacaacctgcgaactgaga 242

Db 412 TACAGTGGGGTCCCGCCGAGCTTCCATTGCGTAGCTAACACCTCGCAACTGGAGA 471

Db 472 GCGGGGGGGCCACGCCGTAATAACACCACTTCTGATGTTGACCTCGAATCAGGTAGCA 531

Db	532	ATACCGCTGA	CTTA	548
27	002	acacccgcgcgaac	ctta	519

RESULT 7
A178308

LOCUS	549 bp	DNA	linear	PLN 20-DEC
DEFINITION	AF178398			
	Nectria ipomoeae strain NRRL22101	185	ribosomal RNA gene, partial	
	sequence: internal transcribed spacer 1	5	95	ribosomal subunit 18S

and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

KEYWORDS
NECTRIA
SOURCE
ORGANISM
Nectria ipomoeae.
101000001 01.10.100025

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.
1 (bases 1 to 549)

AUTHORS O'Donnell, K.
TITLE Molecular phylogeny of the *Fusarium solani* species complex
JOURNAL Unpublished

AUTHORS
 TITLE
 Journal
 Direct Submission
 O'Donnell, K.
 1993

ARS, 1815 N. University St., Peoria, IL 61604, USA
Location/Qualifiers
1
EAO

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/organism="Nectria ipomoeae"
/strain="NRRL22101"
/db xref="taxon:57162"

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musc_rna
<1. .5549
/note="contains 18S ribosomal RNA, internal transcribed
spacer 1, 5.8S ribosomal RNA, internal transcribed spa

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BASE COUNT	142 a	158 c	136 g	113 t
ORIGIN				

Query Match	92.48;	Score 294.6;	DB 8;	Length 549;
Best Local Similarity	92.48;	Score 294.6;	DB 8;	Length 549;

Matches	303;	Conservative	0;	Mismatches	14;	Indels	0;	Gaps	
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Db 233 AAATGCCATAGTATGTGAATTCGAGATTCAGTGAATCATCGAATCTTTGAACGCACA 292

Db 293 TTGCGCCCGCCAGTATTCGTGCGGGGCATGCTGTTCGAGCGTCATTCAACCCCTGAGGCC 352

[illegible]

QY	183	tacaaatgagcggtcccgccgagcgttcacatgttgtagtgcataacccctgcgaactggaga	242
Db	413	TACAACTGGCGGTCCCGCCGACGCTTCATGTGGTAGTAGCTAACACCTCTGCACAACGTGAGA	472
QY	243	gagggcgagccacgcgtaaacaccacactctgaatggttgaactgcgaatcaggtaga	302
Db	473	GCGGGCGCGCCATGGCGGTAAACACCCCAACTTCTGAATGTTGACTCCGAATCAGGTAGA	532
QY	303	ataccgcgtgaactaa 319	
Db	533	ATACCGCGTGAACCTTAA 549	
RESULT	8		
LOCUS	AF178413	546 bp	DNA linear PLN 20-DEC-2001
DEFINITION	Neocosmospora ornamentata strain NRRL22468 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.		
ACCESSION	AF178413		
VERSION	AF178413.1	GI:10180254	
KEYWORDS			
SOURCE	Neocosmospora ornamentata.		
ORGANISM	Neocosmospora ornamentata.		
REFERENCE	Euharvota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neocosmospora.		
AUTHORS	1 (bases 1 to 546)		
TITLE	O'Donnell,K.		
JOURNAL	Molecular phylogeny of the Fusarium solani species complex		
REFERENCE	unpublished		
AUTHORS	2 (bases 1 to 546)		
TITLE	O'Donnell,K.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA,		
AUTHORS	ARS, 1815 N. University St., Peoria, IL 61604, USA		
JOURNAL	Location/Qualifiers		
FEATURES			
source	1..546		
	/organism="Neocosmospora ornamentata"		
	/strain="NRRL22468"		
	/db_xref="taxon:131368"		
misc_RNA	<1..>546		
	/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"		
BASE COUNT	137 a	157 c	134 g
ORIGIN	118 t		
Query Match	90.5%	Score 288.6;	DB 8; Length 546;
Best Local Similarity	96.5%;	Pred. No. 2.9e-69;	
Matches 306; Conservative	0; Mismatches 9;	Indels 2; Gaps 1;	
QY	3	aaatcgataaataatgtaattgcagaatcagaatcagaatcagaatcttgaacgaca	62
Db	233	AAATCGATTAATTAATGTAATTCGACAAATTCAGTGATTCATCGAATCTTTGAACGACA	291
QY	63	ttgcgcgccgcaatattctgcgcggcattgctgttcgagcgatcattacaacctcgaagcc	122
Db	292	TTGCGCCCGCCAGTATCTGCGGGCGCATGCCGTTCGAGCGCATTAACACCCCTCAGGCG	351
QY	123	cccgagcctcgagtggtgggattcggcgagaaacccctcgtgcggcgacaacgcggtcccca	182
Db	352	TCCGGGCGCTGGCGTTGGGATCGGCGAGACCCCGCC--GTGGGACACACGCGTCCCGCA	409
QY	183	tacaaatgagcggtcccgccgagcgttcacatgttgtagtgcataacccctgcgaactggaga	242
Db	410	TACAACTGGCGGTCCCGCCGACGCTTCATGTGGTAGTAGCTAACACCTCTGCACAACGTGAGA	469
QY	243	gagggcgagccacgcgtaaacaccacactctgaatggttgaactgcgaatcaggtaga	302
Db	470	GCGGGCGCGCCATGGCGGTAAACACCCCAACTTCTGAATGTTGACTCCGAATCAGGTAGA	529

QY	303	ataccgcgtgaacttaa	319	
Db	530	ATATCCCGCTGAACCTTAA	546	
RESULT	9			
AF178402				
LOCUS	AF178402	548 bp	DNA	linear
DEFINITION	Fusarium sp. NRRL22354	18S ribosomal RNA gene, partial sequence;		
		internal transcribed spacer 1, 5.8S ribosomal RNA gene, and		
		internal transcribed spacer 2, complete sequence; and 28S ribosomal		
		RNA gene, partial sequence.		
ACCESSION	AF178402			
VERSION	AF178402.1	GI:10180243		
KEYWORDS				
SOURCE				
ORGANISM	Fusarium sp. NRRL22354.			
	Fusarium sp. NRRL22354.			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
AUTHORS	Hypocreales; mitosporic Hypocreales; Fusarium.			
TITLE	O'Donnell,K.			
JOURNAL	Molecular phylogeny of the Fusarium solani species complex			
REFERENCE	unpublished			
AUTHORS	2 (bases 1 to 548)			
TITLE	O'Donnell,K.			
JOURNAL	Direct Submission			
FEATURES	Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA,			
	ARS, 1815 N. University St., Peoria, IL 61604, USA			
source	Location/Qualifiers			
	1..548			
	/organism="Fusarium sp. NRRL22354"			
	/strain="NRRL22354"			
	/db_xref="taxon:131398"			
misc_RNA	<1..>548			
	/note="contains 18S ribosomal RNA, internal transcribed			
	spacer 1, 5.8S ribosomal RNA, internal transcribed spacer			
	2, and 28S ribosomal RNA"			
BASE COUNT	139 a 164 c 133 g 112 t			
ORIGIN				
Query Match	90.3%:	Score 288.2:	DB 8:	Length 548:
Best Local Similarity	98.4%:	Pred. No. 3.8e-69:		
Matches 312:	Conservative 0:	Mismatches 3:	Indels 2:	Gaps 2:
QY	3	aaatgcgaataa	tgtgaatcgaagaatcaggaatc	atcgaatcttgaacgaca 62
Db	234	AAATCGATAGTAA	TGTGAATGGAATTGCAAGATTGAGTATCATCGAATCTTTGTAACGACA 293	
QY	63	ttgcgcgcgcagat	tcttgcgcggcagtcgttctcgagcgatcattacaaccctcagcc 122	
Db	294	TTCGCCCGCCCGCAGTATCTGCGGGCATGCTGTTCGAGCGCATTTACAAACCTTCAGGCC 353		
QY	123	cccgagccttgcggtt	tgggggagatcggcggaagcccccttgcggggaagaacgcccccaaa 182	
Db	354	CCCCGGCCTGCGGCTTGGGGATGCGGGG-AG	CCCCCGGGGGCAG-ACGCGGTCCCCCAAA 411	
QY	183	tacagttgcgcgtctcccg	cgcgaactcccatcttgctagtagctaacacacctcgacaactgaga 242	
Db	412	TACAGTGGGGGTGCCGCGCACACTTCCATTTGCGTGTAGCTAAACACTCGCAACTGGAGA 471		
QY	243	ggcgcgcgagccagcgcgt	taaaaacaccactctgtaatgcttgaactggaatcaggtaga 302	
Db	472	GCGGGCGGCGCCAGCGCGTA	AAAACCCCAACTTCTGAAGCTTGACCTCGAATCAGGTAGGA 531	
QY	303	ataccgcgtgaacttaa	319	
Db	532	ATATCCCGCTGAACCTTAA	548	
RESULT	10			
AF178412				

LOCUS AF178412 547 bp DNA linear PLN 20-DEC-2001
 DEFINITION Neocosmospora africana strain NRRL22436 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF178412
 VERSION AF178412.1 GI:10180253

KEYWORDS Neocosmospora africana.
 Neocosmospora africana.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neocosmospora.

REFERENCE 1 (bases 1 to 547)
 O'Donnell, K.
 TITLE Molecular phylogeny of the Fusarium solani species complex
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 547)
 O'Donnell, K.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA

FEATURES
 source
 1..547
 /organism="Neocosmospora africana"
 /strain="NRRL22436"
 /db_xref="taxon:131367"
 <1..>547
 /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

BASE COUNT 139 a 158 c 132 g 118 t
 ORIGIN

Query Match 90.0%; Score 287; DB 8; Length 547;
 Best Local Similarity 96.2%; Pred. No. 8.1e-69;
 Matches 303; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

QY 3 aaatcgataagtaatgtaattgcagaattcagaattcaatcaatccttgaacgcaca 62
 |||||||
 Db 233 AATGCGATGAATGTAATGCAATTCAGAAATTCAGATCATGAACTTTGAACGCACA 292

QY 63 ttgagccgcagatattctgggggagcattcttcgaagcgttaatacaacctcgaagcc 122
 |||||||
 Db 293 TTGCGCCCGCCAGATATCTGCGCGGCGATGCTTTCAGAGCTCATTAACAACCTTCAGGCC 352

QY 123 ccgagccctggcgttggggagatcgaggaagcccccctggcgacaaagccgtcccca 182
 |||||||
 Db 353 TCCGGGCTTGCGGTGGGAGTCGGAGGCCCC--GTGGCACAAGCCGTCGCCCAAA 410

QY 183 tacagtgagtcgcgcgcgcagcttccatctgcgtagtaagtaaacacctcgaactggaga 242
 |||||||
 Db 411 TACAGTGGCGGTCGCCGCCGATCTTCCATTTGCGTAGTACACTCGCAACTGGAGA 470

QY 243 gcgagcgagcgcacgcgttaaacacacaccttctgaatgttgacctcgaatcagtagaga 302
 |||||||
 Db 471 GCGCGCGGCGCGACGCCGTAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGGA 530

QY 303 ataccgcgtgaactaa 319
 |||||||
 Db 531 ATACCCGCTGAACCTTA 547

RESULT 11
 NEXTS 544 bp DNA linear PLN 17-MAY-1996
 LOCUS Neocosmospora vasinfecta internal transcribed spacer DNA.
 DEFINITION U36627
 VERSION U36627.1 GI:974161
 KEYWORDS PCR primer; internal transcribed spacer; soybean sudden death syndrome.
 SOURCE Neocosmospora vasinfecta (strain NRRL 22166) DNA.
 ORGANISM Neocosmospora vasinfecta

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Neocosmospora.

REFERENCE 1 (bases 1 to 544)
 O'Donnell, K. and Gray, L.E.
 TITLE Phylogenetic relationships of the soybean sudden death syndrome pathogen Fusarium solani f. sp. phaseoli inferred from rDNA sequence data and PCR primers for its identification
 JOURNAL Mol. Plant Microbe Interact. 8 (5), 709-716 (1995)
 MEDLINE 96025088

FEATURES
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 1..544
 /organism="Neocosmospora vasinfecta"
 /strain="NRRL 22166"
 /db_xref="taxon:40622"
 1..544
 /note="internal transcribed spacer"

BASE COUNT 137 a 157 c 133 g 117 t
 ORIGIN

Query Match 89.5%; Score 285.6; DB 8; Length 544;
 Best Local Similarity 96.5%; Pred. No. 2e-68;
 Matches 303; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 3 aaatcgataagtaatgtaattgcagaattcagaattcaatcaatccttgaacgcaca 62
 |||||||
 Db 233 AATGCGATGAATGTAATGCAATTCAGAAATTCAGATCATGAACTTTGAACGCACA 292

QY 63 ttgagccgcagatattctgggggagcattcttcgaagcgttaatacaacctcgaagcc 122
 |||||||
 Db 293 TTGCGCCCGCCAGATATCTGCGCGGCGATGCTTTCAGAGCTCATTAACAACCTTCAGGCC 352

QY 123 ccgagccctggcgttggggagatcgaggaagcccccctggcgacaaagccgtcccca 182
 |||||||
 Db 353 TCCGGGCTTGCGGTGGGAGTCGGAGGCCCC--GTGGCACAAGCCGTCGCCCAAA 410

QY 183 tacagtgagtcgcgcgcgcagcttccatctgcgtagtaagtaaacacctcgaactggaga 242
 |||||||
 Db 411 TACAGTGGCGGTCGCCGCCGATCTTCCATTTGCGTAGTACACTCGCAACTGGAGA 470

QY 243 gcgagcgagcgcacgcgttaaacacacaccttctgaatgttgacctcgaatcagtagaga 302
 |||||||
 Db 471 GCGCGCGGCGCGACGCCGTAACACCACTTCTGAATGTTGACCTCGAATCAGGTAGGA 530

QY 303 ataccgcgtgaact 316
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 Db 531 ATACCCGCTGAACCT 544

RESULT 12
 NEXTS 550 bp DNA linear PLN 20-DEC-2001
 LOCUS AF178406
 DEFINITION Fusarium sp. NRRL22396 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION AF178406
 VERSION AF178406.1 GI:10180247

KEYWORDS Fusarium sp.
 Neocosmospora vasinfecta.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 550)
 O'Donnell, K.
 TITLE Molecular phylogeny of the Fusarium solani species complex
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 550)
 O'Donnell, K.
 TITLE Direct Submission
 JOURNAL Submitted (18-AUG-1999) Microbial Properties Research, NCAUR, USDA, ARS, 1815 N. University St., Peoria, IL 61604, USA

FEATURES
 Location/Qualifiers

source	1. .550 /organism="Fusarium sp. NRRL22396" /strain="NRRL22396" /db_xref="taxon:131402"
misc_RNA	<1. .>550 /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
BASE COUNT	136 a 161 c 133 g 120 t
ORIGIN	
Query Match	87.8%; Score 280.2; DB 8; Length 550;
Best Local Similarity	92.7%; Pred. No. 6.1e-67;
Matches 294:	Conservative 0; Mismatches 23; Indels 0; Gaps 0;
OY	3 aaatcgataaaagtgaattgcaagatcagaatcagaatcgaatctttagacgcaca 62
DB	234 AAAATCGAATAGCTAATTGGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACA 293
OY	63 ttgggccgcccagatattctggcgaggcattgcttcggagcgttcattacaaccttaagcc 122
DB	294 TTGGCCCGCCCGATTCCTTGCGGCGCATGCCGTCTCGAGCCGTCATTACAAACCTCAGGCC 353
OY	123 ccggcgactgagctgttgaggatcggggaagccccctcgcgagcgacacagccgcgcccca 182
DB	354 CCGGCGCCTGGCGGCTTGGGGATGGGGAGAGCCCCCTGGGGCAAAACGCCCTCCCCAAA 413
OY	183 taacagtgcggtccgcgcgcagcttcacattgctgtagtagtaagtaaaccttcgaactggaga 242
DB	414 TTAAGTAGCGGGCTCTGGCTGCACGCTCCATTGGGTGATGACTAACCTTCGCAACTGGAAC 473
OY	243 ggcgagcgagccacgcgcgttaaacaaccacaactctgaatgtgaactggaatcagtagga 302
DB	474 GCCCGCTGGCCATTGCCGTTAAACCCCCAACTTCTGAATGTTTACCTTCGATCAGGTAGGA 533
OY	303 ataccgcgtgaacttaa 319
DB	534 ATACCCGCTGAACTTAA 550
RESULT 13	
AF150466	
LOCUS	AF150466 480 bp DNA linear PLN 05-JAN-2001
DEFINITION	Nectria haematococca strain SUF209 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.
ACCESSION	AF150466
VERSION	AF150466.1 GI:7650164
KEYWORDS	
SOURCE	.
ORGANISM	Nectria haematococca. Nectria haematococca Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.
REFERENCE	1 (bases 1 to 480)
AUTHORS	Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M. Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region
JOURNAL	Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE	2 (bases 1 to 480)
AUTHORS	Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE	Direct Submission
JOURNAL	Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu University, Gifu 501-1112, Japan
FEATURES	Location/Qualifiers
source	1. .480 /organism="Nectria haematococca" /strain="SUF209" /db_xref="taxon:140110" /note="anamorph: Fusarium solani f. sp. radicicola"
misc_RNA	1. .150 /product="internal transcribed spacer 1"
rRNA	151. .308

	misc_RNA	/product="5.8S ribosomal RNA"	
		309 .480	/product="internal transcribed spacer 2"
BASE COUNT	121 a 146 c 116 g 97 t		
ORIGIN			
Query Match	87.5%; Score 279; DB 8; Length 480;		
Best Local Similarity	100.0%; Pred. No. 1.3e-66;		
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	3 aaatcgcataaagtgtgaattgcaagaattcacagaaatcatcgaaattcttgaacgcaca	62	
DB	202 AATTCGATAACTAATGTGAATTGCAGAAATTCAGTAATCAGATCTTGAAACGCACA	261	
OY	63 ttgcgcccccgcagtaattcttgccgggacgatccttgttcgagcgtlcaatlacaacctgaagcc	122	
DB	262 TTGGCCCGGCCAGTATTCGTGGGGGGCATGCCGTGTGCAAGCGTATTACACCCTCAGGCC	321	
OY	123 cccggagccttgagcgtttggaggatctgcggaaagccccctgcgggacacaagccgtcccca	182	
DB	322 CCGGGCCCTGGCGTTGGGAGATCGCGGAAGCCCCCTCGGGCACAAACCGCTCCCCCAA	381	
OY	183 taacaatgagcgtccgcgcgcgcgaactccaattgctgtagtaagtaacaaccctgcgaactgaga	242	
DB	382 TACAGTGGCGGTCGGCGGCACACTTCATTTGGTGTGATGCTAACACCTCGCAACTGGAGA	441	
OY	243 gcggcgaggccacgcgcgtaaaaacaccaactctgaaty	281	
DB	442 GCGGGCGGCCACGCCGTAAAACACCAACTTCTGAAG	480	
RESULT 14			
AF150467			
LOCUS	AF150467 480 bp DNA linear PLN 05-JAN-2001		
DEFINITION	Nectria haematococca strain SUF210 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.		
ACCESSION	AF150467		
VERSION	AF150467.1 GI:7650165		
KEYWORDS			
SOURCE			
ORGANISM	Nectria haematococca. Nectria haematococca Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Nectria.		
REFERENCE	1 (bases 1 to 480) Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M. Phylogenetic analysis of phytopathogenic fungus, Fusarium solani based on the rDNA-ITS region Mycol. Res. 104 (10), 1175-1183 (2000)		
AUTHORS	2 (bases 1 to 480) Suga,H., Hyakumachi,M. and Kageyama,K. Direct Submission Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu University, Gifu 501-1112, Japan		
TITLE	Location/Qualifiers		
JOURNAL			
FEATURES			
source	1..480 /organism="Nectria haematococca" /strain="SUF210" /db_xref="taxon:140110" /note="anamorph: Fusarium solani f. sp. radiclecola"		
misc_RNA	1..150 /product="internal transcribed spacer 1"		
rRNA	151..308 /product="5.8S ribosomal RNA"		
misc_RNA	309..480 /product="internal transcribed spacer 2"		
BASE COUNT	122 a 146 c 115 g 97 t		
ORIGIN			
Query Match	87.5%; Score 279; DB 8; Length 480;		
Best Local Similarity	100.0%; Pred. No. 1.3e-66;		
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:38 ; Search time 594.49 Seconds

(without alignments)
921.287 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319
Sequence: 1 gaaatgcatgaatgaatgt.....ggaataccgcgtgaactaa 319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	319	100.0	319	20	AAV70850	Internal transcrib
2	244.4	76.6	2293	23	AA616211	Fungus genomic DNA
3	241.8	75.8	502	21	AAA61893	Fusarium sp. MF638
4	240.2	75.3	310	20	AAV70851	Internal transcrib
5	240	75.2	561	19	AAV59009	F. avenaceum inter
6	195.2	61.2	582	18	AA65100	T. harzianum IMI 3
7	184.8	57.9	569	16	AA65101	T. harzianum IMI 3
8	183.8	57.6	504	18	AA650400	Fusarium culmorum
9	183.8	57.6	504	19	AAV59028	F. culmorum intern

10	183.8	57.6	504	19	AAV62591
11	180.4	56.6	545	19	AAV59030
12	180.4	56.6	545	19	AAV62593
13	180	56.4	546	19	AAV59007
14	180	56.4	546	19	AAV62596
15	179.6	56.3	569	18	AA65099
16	174.8	54.8	503	16	AA65401
17	174.8	54.8	503	19	AAV59029
18	174.8	54.8	503	19	AAV62592
19	171.4	53.7	504	22	AA508426
20	163.6	51.3	615	22	AA676260
21	156.8	49.2	610	20	AAV90111
22	155	48.6	537	21	AA6291725
23	154.8	48.5	545	16	AA65403
24	145.6	45.6	608	20	AAV90110
25	138.8	43.5	549	21	AA6291723
26	138.8	43.5	549	21	AA6291724
27	134.2	42.1	382	21	AAA72783
28	128.4	40.3	605	20	AAV90108
29	127.8	40.1	553	21	AA6291726
30	127.4	39.9	537	24	ABA01153
31	126.6	39.7	365	20	AAV70847
32	125.8	39.4	617	20	AAV90109
33	125	39.2	587	19	AAV43269
34	123.2	38.6	365	20	AAV70849
35	121.2	38.0	364	20	AAV70846
36	118	37.0	353	16	AA650402
37	118	37.0	568	20	AAV90112
38	115.8	36.3	556	19	AAV59008
39	115.8	36.3	556	19	AAV62594
40	113.8	35.7	640	22	AAH73767
41	112.4	35.2	597	19	AAV43265
42	111.2	34.9	346	19	AAV70868
43	111	34.8	526	22	AAV08427
44	111	34.8	578	24	ABA01155
45	110.6	34.7	618	22	AAH73768

ALIGNMENTS

RESULT	1
ID	AAV70850 standard: DNA: 319 Bp.
AAV70850	
XX	AAV70850:
XX	
DT	26-FEB-1999 (first entry)
DE	Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX	
KW	Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW	Mucor rouxii; M. racemosus; M. plumbeus; A. fumigatus;
KW	M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Fusarium solani.
XX	
PN	MO9850584-A2.
PD	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US08926.
XX	
PR	02-MAY-1997; 97US-0045400.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX	

Fusarium culmorum
F. moniliforme int
Fusarium monilifor
F. poae internal t
Fusarium poae PCR
T. harzianum IMI 3
Fusarium graminear
F. graminearum int
Fusarium transcrib
Internal transcrib
Cordyceps sinensis
Phomopsis viticola
Microdochium nivai
Phomopsis viticola
Rosellinia necatri
Rosellinia necatri
5.8s rRNA gene seq
Eutypella vitis in
Rosellinia necatri
Deuteromycetes pol
Sequence containin
Eutypa lata intern
Sequence of ITS re
Sequence containin
Fusarium monilifor
Diplodia gossypina
M. nivale internal
Microdochium nivai
Guignardia citricia
Sequence of ITS re
Internal transcrib
Deuteromycetes pol
Guignardia citricia

XX	07-NOV-1995:	95ES-0002266.
PR	(CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.	
PA	(OUSA -) UNIV SALAMANCA.	
PI	Garcia Ancha I, Grondona Espana I, Monte Vazquez E;	
XX	WPI: 1997-280728/25.	
XX		
DR	Liquid formulation of Trichoderma harzianum and Trichoderma viride	
PT	strains - are used as biological control agents against diseases of	
PT	plants and plant material and as bioinixiation agents	
XX		
PS	Disclosure: Page 26; 37pp; Spanish.	
XX		
CC	The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA	
CC	gene from the filamentous fungi Trichoderma harzianum strain IMI 352940.	
CC	A novel liquid formulation based on strains of T. harzianum and	
CC	T. viride, has the following composition (%w/v%): 0.1-6 sorbitol;	
CC	0.02-2 K3PO3; 0.05-2 KNO3; 0.002-1 MSO4.7H2O; 0.02-2 (NH4)H2PO4;	
CC	0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;	
CC	0.02-2 manganese; and a biological component comprising at least one of:	
CC	T. harzianum IMI 352939 (3 x 10 ⁵ to 10 x 10 ⁷ conidia/ml), T. harzianum	
CC	IMI 352940 (3 x 10 ⁵ to 10 x 10 ⁷ conidia/ml), T. harzianum IMI 352941	
CC	(3 x 10 ⁵ to 10 x 10 ⁷ conidia/ml), T. harzianum CECT 20179 and/or	
CC	T. viride CECT 20178. The Trichoderma fungi, alone or in combination,	
CC	are used as gene recipients to increase activity of the formulation as a	
CC	biological control agent against diseases of plants and plant material	
CC	and biological entities causing biodegradation, and as a	
CC	bioinixiation (bleaching) agent. It is particularly used e.g. in	
CC	agriculture, forestry and gardening; for controlling microorganisms which	
CC	damage food and its packaging, construction materials, raw materials and	
CC	manufactured products. The antagonistic capacity of the four types of	
CC	T. harzianum and one type of T. viride over other soil fungi makes them	
CC	useful for control of plant diseases. Use of this formulation allows	
CC	reduced application of polluting chemical pesticides and is thus more	
CC	eco-friendly.	
XX		
SO	Sequence 582 BP; 129 A; 178 C; 142 G; 133 T; 0 other;	
Query Match	61.2%; Score 195.2; DB 18; Length 582;	
Best Local Similarity	83.8%; Pred. No. 1.2e-55;	
Matches 268; Conservative	0; Mismatches 48; Indels 4; Gaps 4	
OY	3 aaatgcatgaagtaattgtgaattcagaattcagaattacatcgaaactcttgaacgcaca 62	
DB	264 aaatgcatgaagtaattgtgaattcagaattcagaattcagaattcagaattccttgaacgcaca 323	
OY	63 ttggccgccgcaagtattcttgccgggcatgctcgttcgaagcgtcataaacacctcaggcc 122	
DB	324 ttggccgccgcaagtattcttgccgggcatgctcgttcgaagcgtcataaacacctcaggacc 383	
OY	123 ccgggagccgtgtttgggagatcggcggaagccccctcgcgcgacaaacgctcccaccaaa 182	
DB	304 cctccggc-ccccctggcggtttgggagatcgccctccctcctaaggcggtggcgctctccgaaa 442	
OY	103 tacagttgacgtctccgcgcgcagcttcacattcgtagtagtaatacac-cltcgaactggag 241	
DB	443 tacagttgacgtctccgcgcgcagcttcctctcctgcagtagtttgcacactcgcgatcggag 502	
OY	242 agcgagcgggccac-gcgttaaaacccaactctctg-aatgttgaacctcgaatatgta 299	
DB	503 cgcgagcggtctcacacagccgtttaaacaccaactctctgaatgtagtaccctcgatcagta 562	
OY	300 ggaataccgcgtgaactaa 319	
DB	563 ggaataccgcgtgaactaa 582	

ID	AA675101 standard; DNA: 569 BP.
XX	
AC	AA675101:
XX	
DT	17-FEB-1998 (first entry)
XX	
DE	T. harzianum IMI 352941 5.8 S rRNA gene regions ITS1-ITS4.
XX	
KM	ITS1-ITS4 region: 5.8S rRNA; filamentous fungi; Trichoderma harzianum;
KW	liquid formulation; T. viride; gene recipient; increase activity;
RW	biological control agent; plant disease; biodegradation;
XX	biofixation; leaching; ss.
OS	Trichoderma harzianum strain IMI 352941.
XX	
PM	M09716974-A1.
PD	
XX	15-MAY-1997.
PF	
PR	06-NOV-1996; 96MO-ES00206.
XX	
PA	07-NOV-1995; 95ES-0002266.
XX	
PA	(CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX	(UYSA-) UNIV SALAMANCA.
PI	García Ancha I, Grondona España I, Monte Vazquez E;
DR	WP1: 1997-280728/25.
XX	
PT	Liquid formulation of Trichoderma harzianum and Trichoderma viride
PS	strains - are used as biological control agents against diseases of
XX	plants and plant material and as biofixation agents
XX	
PS	Disclosure: Page 27; 37pp; Spanish.
CC	
CC	The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
CC	gene from the filamentous fungi Trichoderma harzianum strain IMI 352941.
CC	A novel liquid formulation based on strains of T. harzianum and
CC	T. viride, has the following composition (w/v%): 0.1-6 sorbitol;
CC	0.02-2 K3PO ₄ ; 0.05-2 KNO ₃ ; 0.002-1 MgSO ₄ .7H ₂ O; 0.02-2 (NH ₄) ₂ HPO ₄ ;
CC	0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;
CC	0.02-2 manganese; and a biological component comprising at least one of:
CC	T. harzianum IMI 352939 (3 x 10 ⁵ to 10 ⁷ conidia/ml), T. harzianum
CC	IMI 352940 (3 x 10 ⁵ to 10 ⁷ conidia/ml), T. harzianum IMI 352941
CC	(3 x 10 ⁵ to 10 ⁷ conidia/ml), T. harzianum CECT 20179 and/or
CC	T. viride CECT 20178. The Trichoderma fungi, alone or in combination,
CC	are used as gene recipients to increase activity of the formulation as a
CC	biological control agent against diseases of plants and plant material
CC	and biological entities causing biodegradation, and as a
CC	biofixation (leaching) agent. It is particularly used e.g. in
CC	agriculture, forestry and gardening; for controlling microorganisms which
CC	damage food and its packaging, construction materials, raw materials and
CC	manufactured products. The antagonistic capacity of the four types of
CC	T. harzianum and one type of T. viride over other soil fungi makes them
CC	useful for control of plant diseases. Use of this formulation allows
CC	reduced application of polluting chemical pesticides and is thus more
CC	eco-friendly.
XX	
CC	
XX	
SO	Sequence 569 BP; 139 A; 171 C; 143 G; 116 T; 0 other;
Query Match	57.9%; Score 184.8; DB 18; Length 569;
Best Local Similarity	83.4%; Pred. No. 3.7e-52;
Matches 272; Conservative	0; Mismatches 42; Indels 12; Gaps 5;
OY	3 aaatcgataagtaattggaattgcagaattacgaatcagaaactttgaagcaca 62
DB	247 aaatggcataagtaatcgcaattgcagaattacgaatcagaaactttgaagcaca 306
OY	63 ttgcgcccgccagtaattcttgccggaccgaccttcgttcgagcgcatcacaccctcaggcc 122
DB	307 ttgcgcccgccagtaattcttgccggaccgaccttcgttcgagcgcatcacaccctcaggcc 366

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OY 123 cc--cggagcttgcgttttggagctcggcgaagcccccttgcggcaacaagcgcgtccc 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 367 cctccggggggttcggcgtttgggggacctccggagcctcctaagacg---gatccgggcc 423
OY 179 caaatacagtgtgcgttcccgccgagcttccattcgtctagtacgtcaaacctc---gcaa 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 424 gaataacagtgtgcgttcccgccgagcttccctcgtcgcagtgtgttcgacaactcgcgac 483
OY 236 ctgagagagcggcgcgcgaag-ccgtaaacaaccaactctcg-aatgtgtacctgaat 293
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 484 cgggagcgcgcgcgtccacgctccgttaaaacaccaactctctgaatgtgtacctgat 543
OY 294 caggttagaataaccgcgtcgaacttaa 319
Db 544 caggttagaataaccgcgtcgaacttaa 569

```

RESULT 8

ID AAT05400 standard; DNA; 504 BP.

AC AAT05400;

DT 04-JUN-1996 (first entry)

DE Fusarium culmorum internal transcribed spacer sequence.

KW Plant pathogen; *Septoria nodorum*; *Septoria tritici*; *Fusarium*;

KW *Mycosphaerella muscolola*; amplification; primer; ribosomal RNA gene;

KW isolate; development; population; random amplified polymorphic DNA; ss.

OS Fusarium culmorum.
xy

PN W09529260-A2.
XY

02-NOV-1995. PD
xy

PF 19-APR-1995; 95WO-US04712.
XY

PR 25-APR-1994; 9405-02333608.
YY

PA (CIBA) CIBA GEIGY AG.
XX

PI Beck JJ, Ligon JM;
XX

DR WP1; 1995-383005/49.
XX

PT DNA encoding intervening transcribed sequence - used for detection of plant fungal pathogens

XX
PS C:\ajm 1: Page 54-55: 65nn: English

A novel method for the detection of plant pathogenic strains of fungi e.g. *Septoria nodorum*, *S. tritici*, *Pseudocercospora herpotrichoides*, *Mycosphaerella flitensis*, *M. muscicola* or *Puccinia* spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AA094359-93 and AA005357-72. These primers are derived from the ITS sequences of these fungi (AA005394-T05404 and AA094398) and are strain specific. The amplification products of the reactions using these CC primers can be used with the capture primers AA005378-93 in CC colourimetric assays. The primers and ITS DNAs can be used for the CC detection of specific fungal pathogen isolates and in monitoring disease CC development in plant populations.

SQ Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 4 other;

Query Match	57.6%;	Score 183.8;	DB 16;	Length 504;
Best Local Similarity	81.5%;	Pred. NO. 7.7e-52;		

Matches 255; Conservative 1; Mismatches 38; Indels 19; Gaps 3;

[illegible]

RESULT 9

ID AAV59028 standard; DNA; 504 BP.

AC AAV59028;

DT 06-JAN-1999 (first entry)

F. culmorum internal transcribed spacer.

KM Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen
KM fungal pathogen identification; infection identification; ss.

Fusarium culmorum.

FH	Key	Location/Qualifiers

ET

FT	misc_feature	319..472
----	--------------	----------

```

/NOTE= "ITS2"

```

PN US5827695-A.

PD 27-OCT-1998.

PF 01-AUG-1997; 97US-0905314.

PR 01-AUG-1997; 97US-0905314.
VY

PA (NOVS) NOVARTIS FINANCE CORP.
XX

PI Beck JJ;
yy

DR WPI; 1998-593995/50.
YY

Wheat pathogen internal transcribed spacer sequences - used as a basis for primers for the species-specific multiplexed PCR.

PT detection of the pathogens

PS Disclosure; Column 21-22; 20pp; English.
XX

CC This sequence represents an internal transcribed spacer (ITS) sequence ob
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungi


```

DT 06-JAN-1999 (first entry)
XX F. moniliforme internal transcribed spacer.
DE Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KW fungal pathogen identification; infection identification; ss.
XX Fusarium moniliforme.
OS
FH Key Location/Qualifiers
FT misc_feature 31..178
FT /*tag= a
FT /note= "ITS1"
FT misc_feature 336..488
FT /*tag= b
FT /note= "ITS2"
XX
XX US5827695-A.
XX
XX 27-OCT-1998.
XX
XX 01-AUG-1997; 97US-0905314.
XX
XX 01-AUG-1997; 97US-0905314.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JJ:
XX
XX WPI: 1998-593995/50.
XX
XX Wheat pathogen internal transcribed spacer sequences - used as a
XX basis for primers for the species-specific polymerase chain reaction
XX detection of the pathogens
XX
XX Disclosure; Column 23-26; 20pp; English.
XX
XX This sequence represents an internal transcribed spacer (ITS) sequence of
XX the invention. The primer pairs, based on the ITS sequences, are used for
XX the PCR amplification detection of wheat Microdochium and Fusarium fungal
XX pathogens, especially M. nivale, F. graminearum, F. culmorum,
XX F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different
XX strains of fungi show different symptoms during infection, which may or
XX may not be due to infection. Early identification of the strain causing
XX the infection allows early, and more specific fungicidal treatment.
XX
XX Sequence 545 BP; 148 A; 143 C; 125 G; 129 T; 0 other:
XX
Query Match 56.6%; Score 180.4; DB 19; Length 545;
Best Local Similarity 82.4%; Pred. No. 1.1e-50;
Matches 262; Conservative 0; Mismatches 36; Indels 20; Gaps 4;

```

```

OY 302 aataccgcgtgaactaa 319
DB 508 aataccgcgtgaactaa 525

RESULT 12
AAV62593
ID AAV62593 standard; DNA; 545 BP.
XX
XX AAV62593;
XX
XX 17-DEC-1998 (first entry)
XX
XX Fusarium moniliforme PCR amplified ITS region DNA sequence.
XX
XX Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;
XX Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX Septoria avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;
XX PCR; nucleic acid detection; ss.
XX
XX Fusarium moniliforme.
XX
XX Key Location/Qualifiers
FH misc_feature 1..30
FT /*tag= a
FT /note= "3' end of small subunit rRNA gene"
FT misc_feature 31..178
FT /*tag= b
FT /note= "ITS 1"
FT misc_feature 179..335
FT /*tag= c
FT /note= "5.8S rRNA gene"
FT misc_feature 336..488
FT /*tag= d
FT /note= "ITS 2"
FT misc_feature 489..545
FT /*tag= e
FT /note= "5' end of large subunit rRNA gene"
XX
XX US5814453-A.
XX
XX 29-SEP-1998.
XX
XX 02-JUL-1997; 97US-0887480.
XX
XX 02-JUL-1997; 97US-0887480.
XX
XX 19-APR-1995; 95MO-US04712.
XX
XX 15-OCT-1996; 96DS-0722187.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JJ:
XX
XX WPI: 1998-541745/46.
XX
XX DNA isolated from fungal RNA, and its internal transcribed spacer
XX sequence - used for detecting fungal pathogens in plant tissue
XX
XX Claim 2; Fig 3; 56pp; English.
XX
XX This represents the DNA sequence of the internal transcribed spacer (ITS)
XX region that was PCR amplified from Fusarium moniliforme. The invention
XX provides a DNA molecule isolated from the ribosomal RNA gene region of a
XX fungal pathogen, where the DNA molecule consists of an ITS sequence
XX selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum,
XX Fusarium moniliforme, Septoria avenae or Microdochium nivale. A method
XX for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae,
XX F. avenaceum and M. nivale isolates is also provided. The method
XX comprises isolating DNA from a plant leaf infected with at least one of
XX the above pathogens and amplifying parts of the ITS sequence of the
XX pathogen(s) by PCR using specific primers from within these sequences.
XX The pathogen(s) are detected by visualising the amplified part of the
XX ITS sequence.

```



```
FT      /note= "ITS 2"
FT      mls_cfeature 490..546
FT      /tag= e
FT      /note= "5' end of large subunit rRNA gene"
PN      US5814453-A.
PD      29-SEP-1998.
PF      02-JUL-1997; 97US-0887480.
PR      02-JUL-1997; 97US-0887480.
PR      19-APR-1995; 95WO-US04712.
PR      15-OCT-1996; 96US-0722187.
XX      (NOVS ) NOVARTIS FINANCE CORP.
XX      Beck JJ:
XX      WPI: 1998-541745/46.
XX      DNA isolated from fungal RNA, and its internal transcribed spacer
XX      sequence - used for detecting fungal pathogens in plant tissue
XX      Examples: Columns 87-88; 56pp; English.
XX      This represents the consensus DNA sequence of the internal transcribed
XX      spacer (ITS) region that was PCR amplified from Fusarium poae
XX      isolates, T-427, T-534 and T-756. The invention provides a DNA
XX      molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
XX      pathogen, where the DNA molecule consists of an ITS sequence selected
XX      from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX      moniliforme, Septoria avenae or Microdochium nivale. A method for
XX      detecting F. graminearum, F. culmorum, F. moniliforme, F. poae,
XX      F. avenaceum and M. nivale isolates is also provided. The method
XX      comprises isolating DNA from a plant leaf infected with at least one of
XX      the above pathogens and amplifying parts of the ITS sequence of the
XX      pathogen(s) by PCR using specific primers from within these sequences.
XX      The pathogen(s) are detected by visualising the amplified part of the
XX      ITS sequence.
SO      Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 other;

Query Match 56.4%; Score 180; DB 19; Length 546;
Best Local Similarity 82.4%; Pred. No. 1.5e-50;
Matches 262; Conservative 0; Mismatches 35; Indels 21; Gaps 4;

OY      2 aaatgcgataagtaatgtaattgcagaattcgaatcgaatcgaatcgttgaagcgc 61
DB      230 aaatgcgataagtaatgtaattgcagaattcgaatcgaatcgaatcgttgaagcgc 289
OY      62 atgcgcccgcagatcttcgagcgagcagctgctgcagcgtcattacaacctcaagc 121
DB      290 atgcgcccgcagatcttcgagcgagcagctgctgcagcgtcattacaacctcaagc 349
OY      122 ccccgagcctgagctgggagatcgcggaagcccccctgcgggacaaacgcgctcccca 181
DB      350 ccc---agcttggtgtggg-----atcgtgtgcaaacacagctcccca 390
OY      182 atacaatgagctgcgcgcagcttcacatcttgctagtagtcaaacctcgaactgaag 241
DB      391 atgattgagctgcgcgcagctgcg---agcttcacatagctagtaattacaacatgta 449
OY      242 agcgcgagcgagcgaacccaacacacacacacacacacacacacacacacacacac 301
DB      450 atcgttcgagcgagcgaacccaacacacacacacacacacacacacacacacacacac 508
OY      302 aataccgcgtgaactaa 319
DB      509 aataccgcgtgaactaa 526
```

```
RESULT 15
AAT65099
ID      AAT65099 standard; DNA: 569 BP.
XX      AAT65099;
XX      17-FEB-1998 (first entry)
DE      T. harzianum IMI 352939 5.8 S rRNA gene regions ITS1-ITS4.
XX      ITS1-ITS4 region: 5.8S rRNA; filamentous fungi: Trichoderma harzianum;
XX      liquid formulation; T. viride; gene recipient; increase activity;
XX      biological control agent; plant disease; biodegradation;
XX      biolixiviation; leaching; ss.
OS      Trichoderma harzianum strain IMI 352939.
XX      WO9716974-A1.
XX      15-MAY-1997.
XX      06-NOV-1996; 96WO-ES00206.
XX      07-NOV-1995; 95ES-0002266.
XX      (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX      (UYSA-) UNIV SALAMANCA.
XX      Garcia Ancha I, Grondona Espana I, Monte Vazquez E;
XX      WPI: 1997-280728/25.
XX      Liquid formulation of Trichoderma harzianum and Trichoderma viride
XX      strains - are used as biological control agents against diseases of
XX      plants and plant material and as biolixiviation agents
XX      Disclosure: Page 26; 37pp; Spanish.
XX      The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
XX      gene from the filamentous fungi Trichoderma harzianum strain IMI 352939.
XX      A novel liquid formulation based on strains of T. harzianum and
XX      T. viride, has the following composition (w/w%): 0.1-6 sorbitol;
XX      0.02-2 K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4;
XX      0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;
XX      0.02-2 manganese; and a biological component comprising at least one of:
XX      T. harzianum IMI 352939 (3 x 105 to 10 x 107 conidia/ml), T. harzianum
XX      IMI 352940 (3 x 105 to 10 x 107 conidia/ml), T. harzianum IMI 352941
XX      (3 x 105 to 10 x 107 conidia/ml), T. harzianum CECT 20179 and/or
XX      T. viride CECT 20178. The Trichoderma fungi, alone or in combination,
XX      are used as gene recipients to increase activity of the formulation as a
XX      biological control agent against diseases of plants and plant material
XX      and biological entitles causing biodegradation, and as a
XX      biolixiviation (leaching) agent. It is particularly used e.g. in
XX      agriculture, forestry and gardening; for controlling microorganisms which
XX      damage food and its packaging, construction materials, raw materials and
XX      manufactured products. The antagonistic capacity of the four types of
XX      T. harzianum and one type of T. viride over other soil fungi makes them
XX      useful for control of plant diseases. Use of this formulation allows
XX      reduced application of polluting chemical pesticides and is thus more
XX      eco-friendly.
SO      Sequence 569 BP; 138 A; 172 C; 143 G; 116 T; 0 other;

Query Match 56.3%; Score 179.6; DB 18; Length 569;
Best Local Similarity 84.4%; Pred. No. 2.1e-50;
Matches 275; Conservative 0; Mismatches 39; Indels 12; Gaps 6;

OY      3 aaatgcgataagtaatgtaattgcagaattcgaatcgaatcgaatcgttgaagcgc 62
DB      247 aaatgcgataagtaatgtaattgcagaattcgaatcgaatcgaatcgttgaagcgc 306
OY      63 ttgcgcccgcagatcttcgagcgagcagctgctgcagcgtcattacaacctcaagc 122
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:05 ; Search time 5019.06 Seconds

(without alignments)
857,836 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaaatgcgataaagtaatgt.....ggatacccgctgaactaa 319

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : EST:*
1: em_estda:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_iny:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.8	32.2	214	10	BF251183
2	100.2	31.4	213	9	AI209736
3	100.2	31.4	318	9	AI213025
4	92	28.8	120	9	AI132787
5	92	28.8	141	9	AI132787
6	92	28.8	870	12	CNS06K29
7	92	28.8	1004	12	CNS06KGF
8	92	28.8	1043	12	CNS06LUV
9	91.2	28.6	846	12	CNS078E0
10	91.2	28.6	893	12	CNS079EG
11	91.2	28.6	939	12	CNS079KH
12	91.2	28.6	995	12	CNS07A08
13	91.2	28.6	999	12	CNS07730
14	91.2	28.6	1034	12	CNS079X2
15	91.2	28.6	1094	12	CNS076RE
16	91.2	28.6	1098	12	CNS07812
17	90.8	28.5	981	12	CNS0769H

C	18	90.4	28.3	360	12	A2923094
C	19	90.4	28.3	392	12	A2923588
C	20	90.4	28.3	424	12	A2923253
C	21	90.4	28.3	436	12	A0874616
C	22	90.4	28.3	436	12	A0492096
C	23	90.4	28.3	440	12	A2931033
C	24	90.4	28.3	448	12	A2916873
C	25	90.4	28.3	453	12	A0874719
C	26	90.4	28.3	456	12	A2923320
C	27	90.4	28.3	468	12	A0875362
C	28	90.4	28.3	480	12	A2931805
C	29	90.4	28.3	480	12	A0492124
C	30	90.4	28.3	481	12	A0491983
C	31	90.4	28.3	485	12	A0875193
C	32	90.4	28.3	488	12	A2931966
C	33	90.4	28.3	497	12	A0492076
C	34	90.4	28.3	503	12	A2931107
C	35	90.4	28.3	505	12	A0875735
C	36	90.4	28.3	507	12	A0492107
C	37	90.4	28.3	508	12	A2930634
C	38	90.4	28.3	514	12	A0874657
C	39	90.4	28.3	515	12	A2927454
C	40	90.4	28.3	518	12	A2930375
C	41	90.4	28.3	519	12	A0503306
C	42	90.4	28.3	520	12	A0874020
C	43	90.4	28.3	521	12	A0875703
C	44	90.4	28.3	522	12	A0875718
C	45	90.4	28.3	522	12	A2926778

ALIGNMENTS

RESULT 1
LOCUS BF251183 214 bp mRNA linear EST 15-NOV-2001
DEFINITION EST418443 Coccidioides immitis spherule cDNA library Coccidioides immitis cDNA clone CIAD94 5' sequence, mRNA sequence.

ACCESSION BF251183
VERSION BF251183.1 GI:16931326
KEYWORDS
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 214)
AUTHORS Gardner/M.J. and Kirkland,T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES

source location/Qualifiers
1..214
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIAD94"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 46 a 54 c 62 g 52 t
ORIGIN
Query Match 32.2%; Score 102.8; DB 10; Length 214;
Best Local Similarity 84.1%; Pred. No. 2.1e-18;
Matches 116; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

[illegible]

RESULT	3	118 bp	mRNA	linear	EST 19-OCT-1998
LOCUS	A1213025/c				
DEFINITION	y6f01a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library				
ACCESSION	A1213025				
VERSION	A1213025.1	GI:3774967			
KEYWORDS	EST.				
ORGANISM	Emmericella nidulans.				
REFERENCE	Emmericella nidulans.				
AUTHORS	Eukariotes: Fungi: Ascomycota: Pezizomycotina; Eurotiomycetes; Eurotiiales; Trichocomaceae; Emmericella.				
TITLE	1 (bases 1 to 318)				
JOURNAL	Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R. and Roe, B.				
COMMENT	An Aspergillus nidulans EST Database				
	Unpublished (1998)				
	Other ESTs: y6f01a1.r1				
	Contact: Bruce A. Roe, University of Oklahoma, brooeu.edu				
	Department of Chemistry and Biochemistry				
	Advanced Center for Genome Technology, University of Oklahoma				
	620 Parrington Oval, Norman, OK 73019, USA				
	Tel: 405 325 4912				
	Fax: 405 325 7762				
	Email: brooeu.edu				
	We anticipate the future release of the cDNA clones to the Fungal				
	Genetics Stock Center				
	Seq primer: M13-20				
	High quality sequence stop: 265.				
FEATURES	Location/Qualifiers				
source	1..318				
	/organism="Emmericella nidulans"				
	/strain="FGSC A26"				
	/db_xref="taxon:162425"				
	/clone="y6f01a1"				
	/clone_1id="Aspergillus nidulans 24hr asexual				
	developmental and vegetative cDNA lambda zap library"				
	/tissue-type="vegetative mycelia, asexual structures"				
	/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:				
	XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript				
	3' end of cDNA cloned into XhoI site of pBluescript"				
BASE COUNT	69 a 93 c 88 g 68 t				
ORIGIN					
	Query Match	31.48;	Score 100.2;	DB: 9;	Length 318;
	Best Local Similarity	89.38;	Pred. No. 1.3e-17;		
	Matches 108;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;
Oy	3 aaatcgataaagtatgtcatgcatgcagatcagtgatcatcgatcttgaacgcaca 62				
Db	204 AACTCGATTAAGTATGTGATTCGATTCGAGATTCACGATCATTCGAGCTTTGGAACGCACA 145				
Oy	63 ttgcgcccgcagatattctggcggcagcctgctgttcgagcagcgtacataccctcagggc 122				
Db	144 TTGCGCCCCCTCGGCGATTCGCGGGGGGCATGCCCTGTCCGAGCCTCATTTGCTGCCCTCAACCC 85				
Oy	123 c 123				
Db	84 c 84				
RESULT	4	120 bp	mRNA	linear	EST 28-DEC-1998
LOCUS	A1327878/c				
DEFINITION	j0606a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library				
ACCESSION	A1327878				

VERSION	AI327878.1	GI:4064255
KEYWORDS	EST.	
SOURCE	Emericella nidulans.	
ORGANISM	Emericella nidulans.	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiatales; Trichocomaceae; Emericella.	
AUTHORS	1 (bases 1 to 120) Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.	
TITLE	An Aspergillus nidulans EST Database	
JOURNAL	Unpublished (1998)	
COMMENT	Other-ESTs: j0906a1.r1 Contact: Bruce A. Roe, University of Oklahoma, broeeu.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broeeu.edu We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center Seq primer: M13-20.	
FEATURES	Location/Qualifiers	
SOURCE	1..120 /organism="Emericella nidulans" /strain="FGSC A26" /db_xref="taxon:162425" /clone="j0906a1" /clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library" /tissue_type="vegetative mycelia, asexual structures" /note="vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"	
BASE COUNT	28 a 33 c 30 g 29 t	
ORIGIN		
Query Match	28.8%; Score 92; DB 9; Length 120;	
Best Local Similarity	90.7%; Pred. No. 1.6e-15;	
Matches	98; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
Oy	3 aaatcgataagtaatggaattgcagaatcgaatcgaatcgttaagcaca 62 	
Db	109 AACTCGAATTAATGATGCAATTCGAGATTGAGTAATCATCGATCTTTGACGCACA 50 	
Oy	63 ttgcgcgccgcagatattctg9cgggcatgcctgttcgagcgctaatc 110 	
Db	49 TTGCGCCCCCTGCGATTCGCGGGGCGCATGCCGTCCGACGTCATTTGC 2 	
RESULT	5	
AI327879	141 bp mRNA linear EST 28-DEC-1996	
LOCUS	j0906a1.r1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone j0906a1 5', mRNA sequence.	
DEFINITION		
ACCESSION	AI327879	
VERSION	AI327879.1	GI:4064256
KEYWORDS	EST.	
SOURCE	Emericella nidulans.	
ORGANISM	Emericella nidulans.	
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiatales; Trichocomaceae; Emericella.	
AUTHORS	1 (bases 1 to 141) Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.	
TITLE	An Aspergillus nidulans EST Database	
JOURNAL	Unpublished (1998)	
COMMENT	Other-ESTs: j0906a1.f1 Contact: Bruce A. Roe, University of Oklahoma, broeeu.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma	

[illegible]

This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvorum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces fragilis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia anomala*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

```
1. .870
/organism="Saccharomyces servazzii"
/strain="CDS 4311"
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BASE COUNT	ORIGIN	others
214	a 177 c 214 g 260 t	5
misc_reature <1.28/0 /note="part of rDNA repeats" /evidence=not-experimental		

Query Match	28.8%;	Score 92;	DB 12;	Length 870;
Best Local Similarity	90.7%;	Pred. No. 3.8e-15;		
Matches 98; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0

```

0y      3 aaatgcgataagtaatgttgaattcgcgaattcgtgaalcatcgaatctttgaaacgaca 62
        |||||
Db      575 AAATGCCATACGTAATGTGAATTGCAGAAATCCGTGAATCATCGAATCTTTGAACGCACA 634

```

Dy 63 ttgcgcccgccagcatcttcgcygcgatcgttctgagcgatcaaac 110
 | | | | | | | | | | | | | | | | | |
Dd 635 TTGCGCCCTGTGTATTCACAGGGGCATGCCGTTTGAGCCTCATTTC 682

RESULT 7

LOCUS	CNS06KGF	1004 bp	DNA	linear	GSS 17-JUN-2003
DEFINITION	T3 end of clone AT0AA005B03 of library AT0AA from strain CBS 4311 of <i>Saccharomyces servazzii</i> , genomic survey sequence.				

ACCESSION	AL402853
VERSION	AL402853.1
	GI:12162391

SOURCE

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

AUTHORS

TITLE

JOURNAL OF FEBS Lett. 487 (1), 47-51 (2000)

REFERENCE

yeast species for molecular evolution studies

MEDLINE 20584711

Genoscope.
AUTHORS

JOURNAL

Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segeff@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces fragilis*, *Kluyveromyces fragilis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia pastoris*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES	Location/Qualifiers
source	1. .1004

misc_feature	/note="end : T3"	<1. >1004	/note="part of rDNA repeats"	/evidence=not_experimental
BASE COUNT	258 a	211 c	247 g	276 t
ORIGIN				12 others

Query Match	28.8%	Score 92;	DB 12;	Length 1004;
Best Local Similarity	90.7%	Pred. No. 4.1e-15;		
Matches 98; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0

QY 3 aaatgcgataagtaatgtaagtaatgcagaatcagtgaaacacacgaatctcttgaacgcaca 62
|||||
Db 795 AAATGCGATACGTAATGTGAATTGCAGAAATCCGTGAATCATCGAATCTTTGAACGCACA 85

Qy	63 ttgcgccccgaagtattcttgcgcggcgtacctgttcgagcgatcaaac	110
Db	855 TTGCGCCCTGTGATTCACAGGGGCATGCCGTGTGAGCGTCAATTC	9022

RESULT & DISCUSSION

LOCUS	CNS06L0Y	1043 bp	DNA	linear	GSS 17-JUN-2001
DEFINITION	T7 end of clone XAT0AA001G02 of library XAT0AA from strain CBS 4311 of <i>Saccharomyces servazzii</i> , genomic survey sequence.				

ACCESSION	AL404672
VERSION	AL404672.1
GI	12166434

SOURCE

REFERENCE

MEDLINE

AUTHORS

TITLE

JOURNAL.

MEDLINE

AUTHORS
TITLE

Genoscope.
Direct Submission

JOURNAL	Submitted (07-sep-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segrel@genoscope.cns.fr - Web : www.genoscope.cns.fr)					
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces Hansenii var. Hansenii, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.					
FEATURES	Location/Qualifiers					
SOURCE	1..1043					
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	/strain="CBS 4311"					
	/db_xref="taxon:27293"					
	/clone="XAT0AA001G02"					
	/clone_1id="XAT0AA"					
	/note="end : T7"					
misc_feature	<1..>1043					
	/note="part of rDNA repeats"					
	/evidence="not_experimental"					
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ORIGIN						
Query Match	28.8% Score 92; DB 12; Length 1043;					
Best Local Similarity	90.7% Pred. No. 4;le-15;					
Matches	98; Conservative	0; Mismatches	10; Indels	0; Gaps	0;	
Qy	3	aatgcagataagatgtaattcgaaatcgaagaatccagtgaatcatcgaaatttgaacgcaca	62			
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Oy	63	tctggccgccgcaatattcttgccgggcaatgcctgtttcgagcgtcattac	110			
Db	686	TTCGCCCTCTGTGTAATTCACGGGGCCATGCTGTTGAGCGTCATATTC	733			
RESULT	9					
CNS07820	846 bp DNA linear GSS 08-JUL-2001					
LOCUS	T7 end of clone BB0AA025B03 of library BB0AA from strain CBS 4732					
DEFINITION	of Pichia angusta, genomic survey sequence.					
ACCESSION	AL434652					
VERSION	AL434652.1 GI:12218066					
KEYWORDS	GSS.					
SOURCE	Pichia angusta.					
ORGANISM	Pichia angusta.					
REFERENCE	Eukariota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.					
AUTHORS	1 (bases 1 to 846) Blandin,G., Florente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.					
TITLE	Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta					
JOURNAL	FEBS Lett. 487 (1), 76-81 (2000)					
MEDLINE	20584723					
REFERENCE	2 (bases 1 to 846)					
AUTHORS	Souclet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolein-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., deMontigny,J., Dujon,B., Durrens,P., Lepingle,A., Florente,B., Malpertuy,A., Neuvéglise,C., Ozler,Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Douvet,M., Wincker,P. and Weissenbach,J.					
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies					
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)					
MEDLINE	20584711					
REFERENCE	3 (bases 1 to 846)					
AUTHORS	Genoscope.					

FEATURES	COMMENT
Source	<p>Direct Submission</p> <p>Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : sequefr@genoscope.cns.fr - Web : www.genoscope.cns.fr)</p> <p>This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvaturum</i>, <i>Saccharomyces exiguus</i>, <i>Saccharomyces servazzii</i>, <i>Zygosaccharomyces rouxii</i>, <i>Saccharomyces kluyveri</i>, <i>Kluyveromyces thermotolerans</i>, <i>Kluyveromyces lactis</i> var. <i>lactis</i>, <i>Kluyveromyces marianus</i> var. <i>marianus</i>, <i>Pichia angusta</i>, <i>Debaryomyces hansenii</i> var. <i>hansenii</i>, <i>Pichia sorbitophila</i>, <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i>. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.</p> <p>Location/Qualifiers</p> <p>1..846</p> <p>/organism="Pichia angusta"</p> <p>/strain="CBS 4732"</p> <p>/db_xref="taxon:1905"</p> <p>/clone="BB0A025B03"</p> <p>/clone_lib="BB0A"</p> <p>/note="end : 77"</p> <p>misc_feature</p> <p><1..>846</p> <p>/note="part of RNA repeats contains 35S rDNA"</p> <p>/evidence-not_experimental</p> <p>274 a 165 c 188 g 267 t 2 others</p>

Query Match	Similarity	28.6%	Score 91.2	DB 12	Length 846
Best Local	Similarity	82.9%	Pred. No. 6.3e-15		
Matches 116	Conservative	0	Mismatches 23	Indels 1	Gaps 1
Oy	3	aatgcatgaatgaatgcaatgcaagaatcagaatcgaatcgaatcgttgaacgaca	62		
Db	462	AAATGCGATAGCTATATGTAATGCAATTCGATTTTCGTAATCATTAATCTTTGAACGACA	521		
Oy	63	ttggccgccgcatcttctgctgggcatgctgttctgagcgatcattacaacctcaggcc	122		
Db	522	TTGGCCCGCTCGTGGTATTCACAGAGGCATGCCGTGTTGAGCGCATTTTC-CTCTCAACC	580		
Oy	123	cccgagcctgagcgttgggga	142		
Db	581	CTCGGCTTTGGTGGATGGCGCA	600		
RESULT 10					
LOCUS	CNS079EG	893 bp	DNA	linear	GSS 08-JUL-2001
DEFINITION	T7 end of clone BBOAA028D03 of library BBOAA from strain CBS 4732				
ACCESSION	AL435182				
VERSION	AL435182.1				
KEYWORDS	GSS.				
SOURCE	<i>Pichia angusta</i> .				
ORGANISM	<i>Pichia angusta</i> .				
REFERENCE	Enariyola, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; <i>Pichia</i> .				
AUTHORS	1 (bases 1 to 893) Blandin, G., Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F.				
TITLE	Genomic exploration of the hemiascomycetous yeasts: 13. <i>Pichia angusta</i>				
JOURNAL	FEBS Lett. 487 (1), 76-81 (2000)				
MEDLINE	20584723				
REFERENCE	2 (bases 1 to 893)				
AUTHORS	Soucié, J.-L., Aigle, M., Artiguenave, F., Blandin, G., Boivin-Eukhara, M., Bon, E., Brottier, P., Casaregola, S., de Montigny, J., Dujon, B., Durrens, P., Leplingle, A., Llorente, B., Malpertuy, A., Neuvéglise, C., Ozler-Kaliperopoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P., and Weissenbach, J.				

[illegible]

AUTHORS	Soclet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bordin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepinje,A., Llorente,B., Malpertuy,A., Neveglise,C., Ozler-Kalogoropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Weslowski-Louvel,M., Wincker,P. and Weissenbach,J.									
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies									
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)									
MEDLINE	20584711									
REFERENCE	3 (bases 1 to 939)									
AUTHORS	Genoscope.									
JOURNAL	Direct Submission									
TITLE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)									
COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces roullii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.									
FEATURES	Location/Qualifiers									
SOURCE	1..939									
	/organism="Saccharomyces servazzii"									
	/strain="CBS 4311"									
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misc_feature	/note="part of rDNA repeats"									
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Query Match	28.6%; Score 91.2; DB 12; Length 939;									
Best Local Similarity	88.9%; Pred. No. 6.6e-15;									
Matches	96; Conservative 2; Mismatches 10; Indels 0; Gaps 0;									
Qy	3 aaatgcgtatgaatgtgaattgcagaattcagtgatcctcgatcttgaagcagca 62									
Db	AAATCGATAGCTATGGAATGAGAAATTCGGAATCATCGAATCTTGAAACGCACA 706									
Qy	ttgcgcgcgcagatattctgcgcgcgcgcgcgcgtctgcgcgcgtcattac 110									
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VERSION	AL435966.1 GI:12219379									
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SOURCE	Pichia angusta.									
ORGANISM	Pichia angusta									
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REFERENCE	1 (bases 1 to 995)									
AUTHORS	Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.									
TITLE	Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta									
JOURNAL	FEBS Lett. 487 (1), 76-81 (2000)									
MEDLINE	20584723									

KEYWORDS GSS.
SOURCE Pichia angusta.
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 1034)
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.
TITLE Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
REFERENCE 2 (bases 1 to 1034)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boloitin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissensbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 1034)
AUTHORS Direct Submission
TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
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/organism="Pichia angusta"
/strain="CBS 4732"
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misc_feature
/note="part of rDNA repeats
contains 35S rDNA"
/evidence=not_experimental
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Query Match 28.6%; Score 91.2; DB 12; Length 1034;
Best Local Similarity 82.9%; Pred. No. 6.9e-15;
Matches 116; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

Qy 3 aaatgcagataagtaatgtaattgcagaattcagtaattcattgaacgcaca 62
Db 498 AAATGCCATACGTAATGTAATGCAATTTTCGTGAATCATTTGAAACGCACA 439
Qy 63 ttgcgcgcgcagatctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 122
Db 438 TTGCGCCCTCTGTAATTCAGAGGCGCATGCGTGTGAGCGTCATTTC-CCCTCAAAAC 380
Qy 123 ccgc 142
Db 379 CTCGCGTTTGTGATGCGGCA 360
RESULT 15

CNS076RE/C
LOCUS CNS076RE 1094 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BB0A006D05 of library BB0A from strain CBS 4732
ACCESSION AL431760
VERSION AL431760.1 GI:12215174
KEYWORDS GSS.
SOURCE Pichia angusta.
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 1094)
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.
TITLE Genomic exploration of the hemiascomycetous yeasts: 13. Pichia angusta
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
REFERENCE 2 (bases 1 to 1094)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boloitin-Fukuhara,M., Bon,E., Brotlier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissensbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 1094)
AUTHORS Direct Submission
TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source
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/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
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/note="end : T7"
misc_feature
/note="part of rDNA repeats
contains 35S rDNA"
/evidence=not_experimental
BASE COUNT 336 a 269 c 192 g 293 t 4 others
ORIGIN

Query Match 28.6%; Score 91.2; DB 12; Length 1094;
Best Local Similarity 82.9%; Pred. No. 7.1e-15;
Matches 116; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

Qy 3 aaatgcagataagtaatgtaattgcagaattcagtaattcattgaacgcaca 62
Db 819 AAATGCCATACGTAATGTAATGCAATTTTCGTGAATCATTTGAAACGCACA 760
Qy 63 ttgcgcgcgcagatctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 122
Db 759 TTGCGCCCTCTGTAATTCAGAGGCGCATGCGTGTGAGCGTCATTTC-CCCTCAAAAC 701

Oy 123 cccgggcccgtggttgaggga 142
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Db 700 CTCGGGTTTGTGATGAGCA 681

Search completed: August 21, 2002, 21:32:09
Job time: 12508 sec


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RESULT 2
: US-08-905-314A-24
: Sequence 24, Application US/08905314A
: Patent No. 5827695
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: No. 5827695artis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meligs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ. ID NO.: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 561 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: STRAIN: Fusarium avenaceum
: INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note="3' end of small subunit
: OTHER INFORMATION: rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
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: FEATURE:
: NAME/KEY: misc_feature
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: OTHER INFORMATION: /note="5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
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: OTHER INFORMATION: /note="ITS 2"
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: US-08-905-314A-24
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: Query Match 75.2%; Score 240; DB 1; Length 561;
: Best Local Similarity 88.7%; Pred. No. 6,8e-68;
: Matches 287; Conservative 2; Mismatches 27; Indels 7; Gaps

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 Db 291 ATTGCGCGCCGCTGTATTCGGCGCGGCATCCTGTTCAGACGTCATTTCAACCCCTCAACG 350
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 QY 122 ccccgagccttggcgtttgggagatgaggggaagcccccctgggggcaaaagcgcgtcccccac 181
 |||||
 Db 351 CCCCCGGTGTGTGTTGGGATTCGGCTCTGCTCTTMTGGCG-----TGCGGCCCCCGAA 404
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 QY 182 atacagttgagctccgcgcgcgcagcttcattcgttagtgaacacacttcgaacttggag 241
 |||||
 Db 405 ATACATTGGCGGCTTCGCTGACGCTCCATTGCGTACTACTAAACACTTCGCAACTGGAA 464
 |||||
 QY 242 agcgagcgagccacgcgcgttaaacacccaactcttgaaattgaacttcgaatacagttagg 301
 |||||
 Db 465 CGCGCGCGGCGCAATGCGGTAATAC-CCCAATCTCTGAATGTGACCTCGGATCAGGTAGG 523
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 QY 302 aataccgcgtgaactaa 319
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 Db 524 AATACCGGCTGACTTAA 541

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1      RESULT      3
2      US-08-652-127C-6
3      : Sequence 6, Application US/08652127C
4      : Patent No. 5792611
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Richard C. Hamelin
8      : TITLE OF INVENTION: DETECTION OF PLANT
9      : TITLE OF INVENTION: PATHOGEN FUNGI
10     : NUMBER OF SEQUENCES: 10
11     :
12     : CORRESPONDENCE ADDRESSES:
13     : ADDRESSEE: George A. Seaby
14     : ADDRESSEE: Seaby & Maclean
15     : STREET: 880 Wellington Street, Suite 708
16     : CITY: Ottawa
17     :
18     : COUNTRY: Canada
19     :
20     : ZIP: K1R 6K7
21     :
22     : COMPUTER READABLE FORM:
23     : MEDIUM TYPE: 3.5 inch diskette
24     : COMPUTER: IBM PC Compatible
25     : OPERATING SYSTEM: PC-DOS/MS-DOS
26     : SOFTWARE: ASCII
27     :
28     : CURRENT APPLICATION DATA:
29     : APPLICATION NUMBER: US/08/652.127C
30     : FILING DATE: May 23, 1996
31     : CLASSIFICATION: 435
32     :
33     : ATTORNEY/AGENT INFORMATION:
34     : NAME: George A. Seaby
35     : REGISTRATION NUMBER: 24,034
36     : REFERENCE/DOCKET NUMBER: 1898
37     : TELECOMMUNICATION INFORMATION:
38     : TELEPHONE: (613) 232-5815
39     : TELEFAX: (613) 232-5631
40     :
41     : INFORMATION FOR SEQ ID NO: 6:
42     : SEQUENCE CHARACTERISTICS:
43     : LENGTH: 581
44     : TYPE: nucleic acid
45     : STRANDEDNESS: double
46     : TOPOLOGY: linear
47     :
48     : US-08-652-127C-6

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Query Match	66.1%	Score	211	DB	1	Length	581
Best Local Similarity	85.5%	Pred	No. 1	4e-58			
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				Gaps			3
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DB	253	AAATCGAATAAATGTAATTCGAGAAATGAGTAACATCAGCAATTTTGAAGCCACA	312				

OY 63 ttggccgcccagatattctggcgggcgatcgctgttcgagcgatcaataaccctcagcc 122
|||||
DB 313 ttggccgcccagatattctggcgggcgatcgctgttcgagcgatcaataaccctcagcc 372
OY 123 ccggcgctgagcgttgggagatcgcggaagcccgctggcgacacagcgctcccccacaa 182
|||||
DB 373 ccggcgctgagcgttgggagatcgcggaagcccgctggcgacacagcgctcccccacaa 426
OY 183 tacagtgagcgttcccgccgagcttcacatgctgtagtagtaacacctcgcaactggaga 242
|||||
DB 427 TATAGTGGCGGCTGCTGCGTAGTACCTTCTGCTGAGTACACCTCCG---ACTGGAAA 483
OY 243 gggcgcgccgacgcccgcggaacaccccaactctg-aaagttagacctgaaatcagtagg 301
|||||
DB 484 ACAGCGTGCCACGCGCTTAACCCCACTTCTTAAGGTTGACCTCGATCAGGTAGG 543
OY 302 aataccgctgaactaa 319
|||||
DB 544 AATACCGCTGAACCTTAA 561

RESULT 4

US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5815
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-7

Query Match 65.8%; Score 210; DB 1; Length 531;

Best Local Similarity 85.2%; Pred. No. 2,8e-58; Mismatches 37; Indels 10; Gaps 3;

Matches 271; Conservative 0; Mismatches 37; Indels 10; Gaps 3;
OY 3 aatcgataaataatgtaattgcagaatcagtgaaatcagatccttgaagcaca 62
|||||
DB 203 AATGCGATTAATGTAATGTAATGCAAGATTGAGTAATCATGTAATCTTTGAAGCACA 262
OY 63 ttggcgccgacagatattctggcgggcgatcgctgttcgagcgatcaataaccctcagcc 122
|||||
DB 263 TTGCGCGCCGACGATATTCTGGCGGCGCATGCTGTTGAGACGCTCATTTCAACCCCTCAAGCC 322

OY 123 ccggcgctgagcgttgggagatcgcggaagcccgctggcgacacagcgctcccccacaa 182
|||||
DB 323 CC GGCGCTTGGTGTGGAGATNGCCGTGCCCGGGGGG-----CGCCNGCTCTTAA 376
OY 183 tacagtgagcgttcccgccgagcttcacatgctgtagtagtaacacctcgcaactggaga 242
|||||
DB 377 TATAGTGGCGGCTGCTGCGTAGTACCTTCTGCTGAGTACACCTCCG---ACTGGAAA 433
OY 243 gggcgcgccgacgcccgcggaacaccccaactctg-aaagttagacctgaaatcagtagg 301
|||||
DB 434 ACAGCGCGGCGCACGCGCTTAACCCCACTTCTTAAGGTTGACCTCGATCAGGTAGG 493
OY 302 aataccgctgaactaa 319
|||||
DB 494 AATACCGCTGAACCTTAA 511

RESULT 5

US-08-652-127C-8
; Sequence 8, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5815
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-8

Query Match 65.7%; Score 209.6; DB 1; Length 583;

Best Local Similarity 85.5%; Pred. No. 3.9e-58; Mismatches 34; Indels 12; Gaps 3;

Matches 272; Conservative 0; Mismatches 34; Indels 12; Gaps 3;
OY 3 aatcgataaataatgtaattgcagaatcagtgaaatcagatccttgaagcaca 62
|||||
DB 257 AATGCGATTAATGTAATGTAATGCAAGATTGAGTAATCATGTAATCTTTGAAGCACA 316
OY 63 ttggcgccgacagatattctggcgggcgatcgctgttcgagcgatcaataaccctcagcc 122
|||||
DB 317 TTGCGCGCGGACGATATTCTGGCGGCGCATGCTGTTGAGGCTCATTTCAACCCCTCAAGCC 376
OY 123 ccggcgctgagcgttgggagatcgcggaagcccgctggcgacacagcgctcccccacaa 182
|||||

Accession	Sequence	Position
Db	CCCCGGCTTGTTGGGGAGATCGCGAGACCTCCGCGCC-----CGCCGTCCTCTAA	428
Oy	183 tacagtagcgggaccgcgcgcagcttcacatgagctagctaacacctgcgaactgtgaga	242
Db	429 TCTAGTAGCGCTCTCGGCTGTAGCTTCTCTGCGTAGTAGCACACCTCTGC---ACTGGAA	485
Oy	243 ggcgcgcgcgcgcgcgcgttaaacacccaactctcgaatg--tgaacctcgaatcaggtagg	304
Db	486 ACAGCGCGCGCACCGCCGTTAAACCCCAACTCTGAAAGTTTGACCTCGGATCAGGTAGG	545
Oy	302 aataccgcgtgaacttaa 319	
Db	546 AATAACCCGCTGAACCTTA 563	

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: RESULT 6
: US-08-652-127C-5
: Sequence 5, Application US/08652127C
: Patent No. 5792611
: GENERAL INFORMATION:
: APPLICANT: Richard C. Hamelin
: TITLE OF INVENTION: DETECTION OF PLANT
: TITLE OF INVENTION: PATHOGEN FUNGI
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: George A. Seaby
: ADDRESSEE: Seaby & Maclean
: STREET: 880 Wellington Street, Suite 708
: CITY: Ottawa
: COUNTRY: Canada
: ZIP: K1R 6K7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/652.127C
: FILING DATE: May 23, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: George A. Seaby
: REGISTRATION NUMBER: 24,034
: REFERENCE/DOCKET NUMBER: 1898
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (613) 232-5815
: TELEFAX: (613) 232-5831
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 594
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
: US-08-652-127C-5

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Query Match	60.1%	Score	191.6	DB 1	Length	594
Best Local Similarity	83.2%	Pred. No.	2,3e-52			
Matches	268	Conservative	0	Mismatches	44	Indels
					10	Gaps
						4

Qy	3	aatgcgataagtaatcgtgaattgcgaatcagtagaatacagaatcttgaacgaca	62
Db	258	AAATGCGAATAATGTAATGGCAATTCAGTAATCATCGAATCTTTGAAGCACA	317
Qy	63	ttgcgcgccgcagtaattctggcgggcagtcgccgttcgaagcgtcatataacccctaagcc	122
Db	318	TTTGCGCCGCCAGTATCTTGCGGGGAGTCCGTGTTGAGCCGTCATTTCACCCCTCAAGCA	377
Qy	123	cc-----cgggccttgcgctttggggatctgcgcgaagccccccttgcgggcacacagcgctcccc	178
Db	378	CCTTGGGGAGACTTGGTGGTTGGGGAGTCCAGGGGCGTCCTCGGGGTC---GGCGCGTCCCC	434
Qy	179	caataacagttgcggtgccgcgcagcttccatttgcgtatgtagcttaaacacttcgaacty	238

Accession	Sequence	Position
Db	CAAAATCTAGTGGCGGTCTCGCTGAGTCTCTCTGCTAGTAA--ATACACCTCGCTCTGG	492
Oy	gagagcgcgcgcgccgaacgcgtaaaacaccacacttctgaat-gltgacctggaatcagg	297
Db	AGTCTCGGTGGGGCAGCGCCCTAAACCCCAACTTTTTCCTGTGATGACCTCGAATTCAGG	552
Oy	taggaataaccccgctgaacttaa	319
Db	TAGGACTACCGCGCTGAACCTTAA	574

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1 RESULT 7
2 US-08-887-480-82
3 ; Sequence 82, Application US/08887480
4 ; Patent No. 5814453
5
6 GENERAL INFORMATION:
7 APPLICANT: Beck, James J
8 TITLE OF INVENTION: Detection of Fungal Pathogens Us
9 TITLE OF INVENTION: Polymerase Chain Reaction
10 NUMBER OF SEQUENCES: 96
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: No. 5814453artis Corporation
13 STREET: 520 White Plains Road
14 CITY: Tarrytown
15 STATE: NY
16 COUNTRY: USA
17 ZIP: 10591
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: PatentIn Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/887,480
26 FILING DATE:
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/722,187
30 FILING DATE: 15-OCT-1996
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Meigs, J. Timothy
33 REGISTRATION NUMBER: 38,241
34 REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 919-541-8587
37 TELEFAX: 919-541-8689
38
39 INFORMATION FOR SEQ ID NO: 82:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 504 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: DNA (genomic)
46 ORIGINAL SOURCE:
47 ORGANISM: Fusarium culmorum
48 INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
49 INDIVIDUAL ISOLATE: (consensus sequence)
50 FEATURE:
51 NAME/KEY: misc_feature
52 LOCATION: 1..12
53 OTHER INFORMATION: /note= "3' end of small subunit
54 OTHER INFORMATION: rRNA gene"
55 FEATURE:
56 NAME/KEY: misc_feature
57 LOCATION: 13..161
58 OTHER INFORMATION: /note= "ITS 1"
59 FEATURE:
60 NAME/KEY: misc_feature
61 LOCATION: 162..318
62 OTHER INFORMATION: /note= "5.8S rRNA gene"
63 FEATURE:
64 NAME/KEY: misc_feature

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: LOCATION: 319..472
: OTHER INFORMATION: /note="fts 2"
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: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 473..504
: OTHER INFORMATION: /note="5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
:
: OS-08-887-480-82

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Best Local Similarity	81.5%	Pred. No. 7e-50;		
Matches 255; Conservative	1;	Mismatches 38;	Indels 19;	Gaps 3;

[illegible]

RESULT 8
 : Sequence 19, Application US/08905314A
 : Patent No. 5827695
 : GENERAL INFORMATION:
 : APPLICANT: Beck, James J.
 : TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
 : TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: No. 5827695artis Corporation Patent Department
 : STREET: 3054 Cornwallis Road
 : CITY: Research Triangle Park
 : STATE: NC
 : COUNTRY: USA
 : ZIP: 20779-2257
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/905,314A
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Meigs, J. Timothy
 : REGISTRATION NUMBER: 38,241
 : REFERENCE/DOCKET NUMBER: CGC 1944
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (919) 541-8587
 : TELEFAX: (919) 541-8689
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:

? LENGTH: 504 base pairs
 ? type: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? ORIGINAL SOURCE:
 ? ORGANISM: *Fusarium culmorum*
 ? INDIVIDUAL ISOLATE: R-5106, R-5126, and R-5146
 ? INDIVIDUAL ISOLATE: (consensus sequence)

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? OTHER INFORMATION: rRNA gene"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 13..161
? OTHER INFORMATION: /note="ITS 1"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 162..318
? OTHER INFORMATION: /note="5.8S rRNA gene"
?
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: OTHER INFORMATION: /note="ITS 2"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 473..504
: OTHER INFORMATION: /note="5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
: US-08-905-314A-19

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Query Match	57.68;	Score 183.8;	DB 1;	Length 504;
Best Local Similarity	81.58;	Pred. No. 7e-50;		
Matches 255; Conservative	1;	Mismatches 38;	Indels 19;	Gaps 3

QY	2	aaatagatataagtaataatgtatgatctggagaattctgatgtaatcatcatgaaattcttgaacgac	61
Db	211	AAAAAGCATTAAGTAATATGTGAATTGCGAAATTCAGTAATCATGAAATCTTTGAACCCAC	270
QY	62	attggccgcgcagatattctgacgggacatgcctgtctgagcgtcatatcaaccctacgac	121
Db	271	ATTGGGCCCCGCGCAGATATTCTGGCGGCGATGCGCTGTGTGAGCGTATTTCAACCCCTCAGC	330
QY	122	ccccgggcccgcgtcttgggagatcgcgcggaagcccccttcgcggcacaacgcgcgtccccc	181
Db	331	CC---ACGTTGGTGTGGGAGACTG-----CAGTCTGTCTGACACTCCCCAA	372
QY	182	atacagatgagcgtgcccgccgcagcttcattcgtctgtagtgcatacacctcgcgaactggag	241
Db	373	ATACATATTGGCGGTACGTCGTAAGCTTCATAGCTAGTAATTTTACATATGGTTACTGTGA	432
QY	242	agcggcgcgcgcacagcgcgttaaacaccccaacttctgaatgttgccttcgatacggtagg	301
Db	433	ATCGTCGGGGCGCACCCGCTTAAC-CCCAACTCTGATGATTTGACCTCGGATCAGGTAGG	491
QY	302	ataccgcgctgaa	314
Db	492	AATTACCCTGCTGAA	504

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1      RESULT          9
2      US-08-722-187-82
3      ; Sequence 82, Application US/08722187
4      ; Patent No. 5955274
5      ;
6      ; GENERAL INFORMATION:
7      ;
8      ; APPLICANT: Ligon, James M
9      ; APPLICANT: Beck, James J
10     ;
11     ; TITLE OF INVENTION: Detection of Fungal Pathogens using the
12     ; POLYMERASE CHAIN REACTION
13     ;
14     ; NUMBER OF INVENTIONS: 86
15

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Db	409	GGGCTCTCGCTCAGCTTCATTCATTCGGCTAGTAGTATAAAACCCCTGCAACATGCTACGGGGCGC	468
0Y	241	ggcgaagccgcttaaaaccccaactctcgaagtctgaactcggatcagtgtaggaataaccg	300
Db	468	GGCCACAGCCGTTAAACCCCAACTTCTGATGTTTGACCTCGGATCAGGTAGGAATACCG	528
0Y	301	ctgaac	306
Db	529	CTGAAC	534

FEATURES	source
LOCUS	FPJ34558 534 bp DNA
DEFINITION	Fusarium proliferatum NRRL 22944 linear
ACCESSION	U34558 internal transcribed spacer RNA.
VERSION	U34558.1 GI:1808934
KEYWORDS	
SOURCE	
ORGANISM	Fusarium proliferatum.
REFERENCE	Fusarium proliferatum
TITLE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocerales; Nectriaceae; Gibberella; Gibberella fujikuroi complex 1 (bases 1 to 534)
REFERENCE	O'Donnell, K. and Cigelnik, E.
TITLE	Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus Fusarium are nonorthologous
REFERENCE	Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
JOURNAL	97159566
MEDLINE	2 (bases 1 to 534)
REFERENCE	O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.
AUTHORS	Molecular systematics and phylogeography of the Gibberella
TITLE	fujikuroi species complex
JOURNAL	Mycologia 90 (3), 465-493 (1998)
REFERENCE	3 (bases 1 to 534)
AUTHORS	O'Donnell, K. and Cigelnik, E.
TITLE	Direct Submission
JOURNAL	Submitted (21-AUG-1995) Kerry O'Donnell, NCAR, USDA, 1815 N.
FEATURES	University St., Peoria IL 61604, USA
source	Location/Qualifiers
	1. 534
	/organism="Fusarium proliferatum"
	/strain="NRRL 22944"
	/db_xref="taxon:42674"
	1. 534
	/product="internal transcribed spacer"
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ORIGIN	

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Best Local Similarity	99.3%	Pred. No. 8	4e-83	
Matches 304	Conservative	0	Mismatches 2	Indels 0
				Gaps 0
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DB	229 AATGCGATAAATGTAATGTAATTGCAGATTGCAGTAATCATCGAATCTTTGAACGCACA	288		
QY	61 ttgcgcgcgcgaagtattctcgcgcgcacatgcctcgttcgaacgcacattcaacccctaagcc	120		
DB	289 TTGCGCGCCCGCATATTCTGCGCGGCATCCTGTTGAGCGTCATTTCAAACCTCAAGC	348		
QY	121 ccgcggtttgtgttttgaggatctgcgaacgcctctgcgcgaacgcgcgcgcgaatctagt	180		
DB	349 CCCGGGTTTGATTGGGATCGCGCAGCCCTTGCGCGAAGCGCGCCCGGAATCTAGTG	408		
QY	181 gcgcgtctgcctcagcttccatcttgtagttaaaccctcgcgaactgcgtgacgcgcgc	240		
DB	409 CGCGTTCGCTCGACCTTCCATTGCTAAGTAAACCTCGCAACTGTAACGGCGGCC	468		
QY	241 ggcacgaacgcgttaaaccaccaatcttgatgttgacctcgcgatcaagttaggaataccg	300		
DB	469 GGCCAAGCGGTTAAACCCCAACTTCTGAATGTGACCTCGGATCGATGAGGAATAACCG	528		

QY	301	ctgaac	306
Db	529	CTGAAC	534

RESULT	13
FAU61670	
LOCUS	534 bp DNA linear PLN 15-JUL-1998
DEFINITION	Fusarium annulatatum internal transcribed spacer ribosomal RNA.
ACCESSION	U61670
VERSION	U61670.1 GI:3320344

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ORGANISM
Fusarium annulatum
Euxairytas: Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
1 (bases 1 to 534)
REFERENCE
O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.,
AUTHORS
Molecular systematics and phylogeography of the Gibberella
TITLE
fujikuroi species complex
JOURNAL
Mycologia 90 (3), 465-493 (1998)
REFERENCE
2 (bases 1 to 534)
AUTHORS
O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.,
TITLE
Direct Submission
JOURNAL
Submitted (21-JUN-1996) USDA/ARS/NCAUR, 1815 N. University, Peoria,
IL 61604, USA

FEATURES
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Location/Qualifiers
1..534
/organism="Fusarium annulatum"
/strain="NRRL13614"
/db_xref="taxon:48484"
misc-RNA
1..534
/note="internal transcribed spacer"
BASE COUNT
135 a 148 c 130 g 121 t
ORIGIN

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[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	RESULT 14
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REFERENCE	2 (bases 1 to 502)
AUTHORS	Iwen,P.C., Henry,T. and Hnichs,S.H.
TITLE	Direct Submission
JOURNAL	Submitted (07-JUN-1999) Pathology and Microbiology, University of Nebraska Medical Center, 986485 Nebraska Medical Center, Omaha, NE 68198-6495, USA
FEATURES	Location/Qualifiers
source	1..502
	/organism="Gibberella fujikuroi"
	/strain="ATCC48843"
	/variety="intermedium"
	/db_xref="ATCC:48843"
	/db_xref="taxon:5127"
	/note="anamorph: Fusarium moniliforme"
	1..147
	/note="ITS1"
	/product="internal transcribed spacer 1"
	148..304
	/product="5.8S ribosomal RNA"
	305..470
	/product="internal transcribed spacer 2"
	471..>502
	/product="28S ribosomal RNA"
BASE COUNT	127 a 141 c 121 g 113 t
ORIGIN	
Query Match	97.0%; Score 300.8; DB 8; Length 502;
Best Local Similarity	99.3%; Pred. No. 3.5e-82;
Matches 302; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
0Y	1 aatcgatagtaatgtggaattcgaaattcaatgaatcatcgaaatttgaaagcaca 60
Db	199 AATCGATAAGTAAATTCGAATTCGAGAAATTCAGTGAATCATGAAATCTTTGAACGCACA 258
0Y	61 ttgcgcgcgcgaatcttcgtgcggcgatgctgttcgagcgatcaattcaaccctcaagcc 120
Db	259 TTGCGCGCGCGAGTATCTGTGGCGGGCAGTCCCTGTTCCAGCGCTATTTCMAACCTCAAGCC 318
0Y	121 cccgggttgatgtgtgggagatcggcaagccttcggcaagcggcccgaaatctagt 180
Db	319 CCGGGGTTGGTGTGGGGATCGGGAGACCCCTTCGGCGCAAGCCGCGCCCAAAATCTAGTG 378
0Y	181 gcggtctcgtcgaacttcattgcgtagtagtaaaacctcgaaactggtgacggcgcc 240
Db	379 GCGGCTCGCTGCGCACTTCATTCGCTGATGTAATAACCTTCGGAAGCTGGTACGGCGGCGC 438
0Y	241 ggcgaagcgcgttaaaccccccaactctgaatgattgacctggatcaggttagaaatccg 300
Db	439 GGCCAAGCGGTTAAACCCCAACTTTCGAATGTTGACCTCGATCAGGTAGGAATACCG 498
0Y	301 ctga 304
Db	499 CTGA 502

Search completed: August 21, 2002, 22:09:49
Job time: 14203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:40 ; Search time 594.49 Seconds
(without alignments)
895.294 Million cell updates/sec

Title: US-10-046-955-7
310

Sequence: 1 aatgcgataagtaatgtga.....ggaataccgcgtgaactaa 310

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.GeneSeq_032802:*

- 1: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1980.DAT:*
- 2: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT:*
- 5: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1984.DAT:*
- 6: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1985.DAT:*
- 7: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1986.DAT:*
- 8: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1987.DAT:*
- 9: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1988.DAT:*
- 10: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1991.DAT:*
- 13: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1992.DAT:*
- 14: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1993.DAT:*
- 15: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1994.DAT:*
- 16: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1995.DAT:*
- 17: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1996.DAT:*
- 18: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1997.DAT:*
- 19: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310	100.0	310	20 AAV70851	Internal transcrib
2	305.8	99.0	2293	23 AAS16211	Fungus genomic DNA
3	265.8	85.7	502	21 AAV61893	Fusarium sp. MF638
4	249.8	80.6	561	19 AAV53009	F. avenaceum inter
5	240.2	77.5	319	20 AAV70850	Internal transcrib
6	193.4	62.4	582	18 AAT65100	T. harziarum IMI 3
7	187.6	60.5	546	19 AAV59007	F. poae internal t
8	187.6	60.5	546	19 AAV62596	Fusarium poae PCR
9	186.6	60.2	504	16 AAT05400	Fusarium culmorum

10	186.6	60.2	504	19 AAV59028	F. culmorum intern
11	186.6	60.2	504	19 AAV62591	Fusarium culmorum
12	185	59.7	610	20 AAY90111	Phomopsis viticola
13	183.2	59.1	545	19 AAV59030	F. moniliforme int
14	183.2	59.1	545	19 AAV62593	Fusarium monilifor
15	180.4	58.2	503	16 AAT05401	F. graminearum int
16	180.4	58.2	503	16 AAV59029	F. graminearum int
17	180.4	58.2	503	16 AAV59029	Fusarium graminear
18	175	56.5	569	18 AAT65101	T. harziarum IMI 3
19	174.2	56.2	504	22 AAS08426	Internal transcrib
20	168.2	54.3	569	18 AAT65099	T. harziarum IMI 3
21	166.2	53.6	545	16 AAT05403	Microdochium nivai
22	163.8	52.8	608	20 AAY90110	Phomopsis viticola
23	157.8	50.9	537	21 AAZ91725	Rosellinia necatri
24	149.4	48.2	615	22 AAT62600	Cordyceps sinensis
25	147.8	47.7	549	21 AAZ91723	Rosellinia necatri
26	147.8	47.7	549	21 AAZ91724	Rosellinia necatri
27	141.8	45.7	382	21 AAY72783	5.8s rRNA gene seq
28	139	44.8	605	20 AAY90108	Eutypella vitis in
29	137.6	44.4	537	24 ABA01153	Deuteromycetes pol
30	136	43.9	365	20 AAV70847	Sequence containin
31	136	43.9	587	19 AAV43269	Sequence of ITS re
32	136	43.9	617	20 AAY90109	Eutypa lata intern
33	134.8	43.5	553	21 AAZ91726	Rosellinia necatri
34	131.4	42.4	364	20 AAV70846	Sequence containin
35	126.6	40.8	556	20 AAZ22438	Internal transcrib
36	126	40.6	640	22 AAT73767	Guignardia citricol
37	125.2	40.4	627	19 AAO94398	P. herpotrichoides
38	125.2	40.4	627	19 AAV62572	P. herpotrichoides
39	125	40.3	309	20 AAV70872	Internal transcrib
40	124.4	40.1	556	19 AAV59008	M. nivale internal
41	124.4	40.1	556	19 AAV62594	Microdochium nivai
42	124.4	40.1	580	19 AAV43268	Sequence of ITS re
43	123.6	39.9	626	16 AAT05396	P. herpotrichoides
44	123.6	39.9	626	19 AAT05396	P. herpotrichoides
45	123.6	39.9	626	19 AAT62503	Internal transcrib

ALIGNMENTS

RESULT	ID	AAV70851	standard; DNA; 310 BP.
XX	AAV70851		
XX	AAV70851		
AC	AAV70851		
XX	26-FEB-1999	(first entry)	
DE	Internal transcribed spacer 2 (ITS2) and adjacent regions.		
XX	Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;		
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;		
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;		
KW	M. circinellii; M. circinellioidei; Rhizopus oryzae; R. microsporus;		
KW	R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;		
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;		
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.		
XX			
OS	Fusarium moniliforme.		
PN	WO9850584-A2.		
XX	12-NOV-1998.		
PD			
PF	01-MAY-1998;	98WO-US08926.	
XX			
PR	02-MAY-1997;	97US-0045400.	
XX			
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
XX			
PI	Aldorevich L, Choi JS, Morrison CJ, Reiss E;		

QY 241 ggcgaagcgttaaaccccaactctgtaattgtgacctcgatcagtgagaataccg 300
 |||
 Db 2212 ggcgaagcgttaaaccccaactctgtaattgtgacctcgatcagtgagaataccg 2271
 |||
 QY 301 ctgacctaa 310
 |||
 Db 2272 ctgacctaa 2281

RESULT 3
 AAA61893
 ID AAA61893 standard: DNA: 502 BP.
 XX
 AC AAA61893:
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE Fusarium sp. MF6381 rdna internal transcribed spacer (ITS) region.
 XX
 KM Ribosomal DNA: rdna ITS region: internal transcribed spacer; ATCC 74469;
 KM HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
 KM acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
 KM symptomatic infection; asymptomatic infection; potential HIV exposure;
 KM combination therapy; ds.
 XX
 OS Fusarium sp. MF6381.
 XX
 PN WO200036132-A1.
 XX
 PD 22-JUN-2000.
 XX
 PF 09-DEC-1999: 99WO-US29356.
 XX
 PR 14-DEC-1998: 98US-0112168.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Singh SR, Zink DL, Hazuda DJ, Felock PJ, Polishook JD:
 PI Dombrowski AM;
 XX
 DR MPI: 2000-431606/37.
 XX
 PT New steroid compounds are HIV integrase inhibitors used for treating
 PT HIV infection and AIDS -
 XX
 PS Disclosure: Page 14; 113pp: English.
 XX
 CC The invention relates to novel steroid compounds derived from the
 CC African soil fungus Fusarium sp. MF6381 (ATCC 74469) which act as
 CC inhibitors of HIV integrase. The invention encompasses cultures of
 CC Fusarium sp. MF6381. The invention also relates to a composition
 CC comprising a compound of the invention in combination with an AIDS
 CC antiviral agent, an immunomodulator and an anti-infective agent. The
 CC compounds of the invention may be used in the inhibition of HIV
 CC integrase and in the prevention and treatment of HIV infection. A wide
 CC range of state of HIV infection may be treated: AIDS (acquired
 CC immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic
 CC and asymptomatic HIV infection; and actual or potential exposure to HIV.
 CC The compounds may be used to isolate HIV integrase mutants which are
 CC potentially useful as screening tools for antiviral compounds. The
 CC compounds may also be used to establish or determine the site at which
 CC other antivirals bind to HIV integrase (e.g., by competitive inhibition).
 CC The present sequence represents the ribosomal DNA (rdna) internal
 CC transcribed spacer (ITS) region of Fusarium sp. MF6381, which may be used
 CC to characterize MF6381.
 CC
 XX
 PS Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 other;

Query Match 85.7%; Score 265.8; DB 21; Length 502;
 Best Local Similarity 93.8%; Pred. No. 8.9e-83;
 Matches 288; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 1 aaatgcgataagtaatgtaattgcaaaattcagtgaaatcagtaattcttgaacgcaca 60
 |||
 Db 196 aaatgcgataagtaatgtaattgcaaaattcagtgaaatcagtaattcttgaacgcaca 255
 |||
 QY 61 ttgcgccgccgcaattcttgcgggcatgctgttcgagcgatcaattcaaccctcaagc 120
 |||
 Db 256 ttgcgccgccgcaattcttgcgggcatgctgttcgagcgatcaattcaaccctcaagc 315
 |||
 QY 121 cccgggttggtgttggggtatcgcaagccct--tgcggaagccgggccccaattcag 178
 |||
 Db 316 cccgggttggtgttggggtatcgcaagccct--tgcggaagccgggccccaattcag 375
 |||
 QY 179 tggcggtctgcgtcagcttccattgcgtagtaaaacctcgcaacttgtaacgcgac 238
 |||
 Db 376 tggcggtctgcgtcagcttccattgcgtagtaaaacctcgcaacttgtaacgcgac 435
 |||
 QY 239 ggcgcaagcgttaaaccccaactctgtaattgtgacctcgatcagtgagaatacc 298
 |||
 Db 436 ggcgcaagcgttaaaccccaactctgtaattgtgacctcgatcagtgagaatacc 495
 |||
 QY 299 cgcgtgaa 305
 |||
 Db 496 cgcgtgaa 502

RESULT 4
 AAV59009
 ID AAV59009 standard: DNA: 561 BP.
 XX
 AC AAV59009:
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE F. avenaceum internal transcribed spacer.
 XX
 DE F. avenaceum internal transcribed spacer.
 XX
 KM Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
 KM fungal pathogen Identification; Infection Identification; ss.
 XX
 OS Fusarium avenaceum.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 31..181
 FT /*tag= a
 FT /note= "ITS1"
 FT 339..504
 FT /*tag= b
 FT /note= "ITS2"
 XX
 PN US5827695-A.
 XX
 PD 27-OCT-1998.
 XX
 PF 01-AUG-1997: 97US-0905314.
 XX
 PR 01-AUG-1997: 97US-0905314.
 XX
 PA (NOVS) NOVARTIS FINANCE CORP.
 XX
 PI Beck JJ;
 XX
 DR MPI: 1998-593995/50.
 XX
 PT Wheat pathogen internal transcribed spacer sequences - used as a
 PT basis for primers for the species-specific polymerase chain reaction
 PT detection of the pathogens
 XX
 PS Claim 1: Column 29-30; 20pp: English.

This sequence represents an internal transcribed spacer (ITS) sequence of
 the invention. The primer pairs, based on the ITS sequences, are used for
 the PCR amplification detection of wheat Microdochium and Fusarium fungal
 pathogens, especially M. nivale, F. graminearum, F. culmorum,

CC F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.
XX
SQ Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 3 other:

Query Match 80.6%; Score 249.8; DB 19; Length 561;
Best Local Similarity 91.6%; Pred. No. 3,7e-77;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;

0Y 1 aaatgagtaagtaatggaattcgaataaattcaatgaatcgcgaatccttgaacgaca 60
DB 232 aaatgagtaagtaatggaattcgaataaattcaatgaatcgcgaatccttgaacgaca 291
0Y 61 ttgagccgagcaatctgagcgagcctgttcgagcgatcattcaaccctcaagcc 120
DB 292 ttgagccgagcaatctgagcgagcctgttcgagcgatcattcaaccctcaagcc 351
0Y 121 ccgaggttggtgttggtgagatcggaagcccttgagc-aagccgagccgaaatcagt 179
DB 352 ccgaggttggtgttggtgagatcggaagcccttgagc-aagccgagccgaaatcagt 411
0Y 180 ggcggttcggtcgcagcttcgagcgttagtaaaacctcgcaactgtgaagcgag 239
DB 412 ggcggttcggtcgcagcctccatctgagtaagtaaacctcgcaactgtgaagcgag 471
0Y 240 ggcgagcagcgcttaaaccccaactctgaatgttgagcctcgagtaggaataccc 299
DB 472 ggcgagcagcg-aaaaccccaactctgaatgttgagcctcgagtaggaataccc 530
0Y 300 gctgaacttaa 310
DB 531 gctgaacttaa 541

RESULT 5
AAV70850
ID AAV70850 standard; DNA: 319 BP.

AC AAV70850;

DT 26-FEB-1999 (first entry)

XX Internal transcribed spacer 2 (ITS2) and adjacent regions.

XX Internal transcribed spacer 2 (ITS2) and adjacent regions.
KM A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KM Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KM M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KM R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KM Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KM Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.

OS Fusarium solani.

PN MO9850584-A2.

PD 12-NOV-1998.

PF 01-MAY-1998; 98MO-US08926.

PR 02-MAY-1997; 97US-0045400.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Aldorevich L, Choi JS, Morrison CJ, Reiss E;

XX WPI: 1999-034737/03.

PT New nucleic acid probes for filamentous fungi - for detecting e.g.
Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,

PT Cunninghamella, Pseudallesheria boydii, Penicillium and Sporothrix
PT species.

XX Claim 1; Page 12; 45pp; English.

CC The present sequence represents an internal transcribed spacer 2 (ITS2)
CC and adjacent regions. Probes can be derived from the present sequence
CC which are species-specific. The specification also describes ITS2
CC sequence-derived probes for identifying a species selected from
CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC M. indicus, M. circinelloides f. circinelloides, Rhizopus oryzae,
CC Absidia corymbifera, Cunninghamella elegans, Pseudallesheria boydii
CC (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.

SQ Sequence 319 BP; 77 A; 96 C; 84 G; 62 T; 0 other;

Query Match 77.5%; Score 240.2; DB 20; Length 319;
Best Local Similarity 87.4%; Pred. No. 6,6e-74;
Matches 277; Conservative 0; Mismatches 33; Indels 7; Gaps 1;

0Y 1 aaatgagtaagtaatggaattcgaataaattcaatgaatcgcgaatccttgaacgaca 60
DB 3 aaatgagtaagtaatggaattcgaataaattcaatgaatcgcgaatccttgaacgaca 62
0Y 61 ttgagccgagcaatctgagcgagcctgttcgagcgatcattcaaccctcaagcc 120
DB 63 ttgagccgagcaatctgagcgagcctgttcgagcgatcattcaaccctcaagcc 122
0Y 121 ccgaggttggtgttggtgagatcggaagcccttgagc-aagccgagccgaa 173
DB 123 ccgaggttggtgttggtgagatcggaagcccttgagc-aagccgagccgaa 182
0Y 174 tctagtgagcgttcgagcgttcgagcgttagtaaaacctcgcaactgtgaagcgag 233
DB 183 tctagtgagcgttcgagcgttcgagcgttagtaaaacctcgcaactgtgaagcgag 242
0Y 234 ggcgagcagcgcaatctgagcgagcctgttcgagcgatcattcaaccctcaagcc 293
DB 243 ggcgagcagcgcaatctgagcgagcctgttcgagcgatcattcaaccctcaagcc 302
0Y 294 ataccgctgaactaa 310
DB 303 ataccgctgaactaa 319

RESULT 6
AAT65100
ID AAT65100 standard; DNA: 582 BP.

AC AAT65100;

DT 17-FEB-1998 (first entry)

DE T. harzianum IMI 352940 5.8 S rRNA gene regions ITS1-ITS4.

XX ITS1-ITS4 region; 5.8S rRNA; filamentous fungi; Trichoderma harzianum;
XX liquid formulation; T. viride; gene recipient; increase activity;
XX biological control agent; plant disease; biodegradation;
XX bioinhibition; leaching; ss.

OS Trichoderma harzianum strain IMI 352940.

PN WO9716974-A1.

XX 15-MAY-1997.

PF 06-NOV-1996; 96MO-ES00206.

XX 07-NOV-1995: 956S-0002266.
PR (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PA (UYSA-) UNIV SALAMANCA.
PI Garcia Ancha I, Grondona Espana I, Monte Vazquez E;
XX MPI, 1997-280728/25.
XX
XX Liquid formulation of *Trichoderma harzianum* and *Trichoderma viride*
PT strains - are used as biological control agents against diseases of
PT plants and plant material and as bioinixivation agents
XX
PS Disclosure: Page 26; 37pp; Spanish.
XX
XX The present sequence represents the ITS1-ITS4 region of the 5.8S rRNA
CC gene from the filamentous fungi *Trichoderma harzianum* strain IMI 352940.
CC A novel liquid formulation based on strains of *T. harzianum* and
CC *T. viride*, has the following composition (w/v%): 0.1-6 sorbitol;
CC 0.02-2 K3PO3; 0.05-2 KNO3; 0.002-1 MgSO4.7H2O; 0.02-2 (NH4)H2PO4;
CC 0.02-2 copper; 0.02-2 zinc; 0.02-2 molybdenum; 0.02-1 boron; 0.02-1 iron;
CC 0.02-2 manganese; and a biological component comprising at least one of:
CC *T. harzianum* IMI 352939 (3 x 105 to 10 x 107 conidia/ml), *T. harzianum*
CC IMI 352940 (3 x 105 to 10 x 107 conidia/ml), *T. harzianum* IMI 352941
CC (3 x 105 to 10 x 107 conidia/ml), *T. harzianum* CECT 20179 and/or
CC *T. viride* CECT 20178. The *Trichoderma* fungi, alone or in combination,
CC are used as gene recipients to increase activity of the formulation as a
CC biological control agent against diseases of plants and plant material
CC and biological entities causing biodegradation, and as a
CC bioinixivation (leaching) agent. It is particularly used e.g. in
CC agriculture, forestry and gardening; for controlling microorganisms which
CC damage food and its packaging, construction materials, raw materials and
CC manufactured products. The antagonistic capacity of the four types of
CC *T. harzianum* and one type of *T. viride* over other soil fungi makes them
CC useful for control of plant diseases. Use of this formulation allows
CC reduced application of polluting chemical pesticides and is thus more
CC eco-friendly.
XX
XX Sequence 582 BP; 129 A; 178 C; 142 G; 133 T; 0 other;
SQ

Query Match 62.4%; Score 193.4; DB 18; Length 582;
Best Local Similarity 85.9%; Pred. No. 26-57;
Matches 274; Conservative 0; Mismatches 36; Indels 9; Gaps 5

0Y 1 aatcgataaagtaatgataatgcgaataatcagtaatcatcgaattttgaacgaca 60
Db 264 aatcgataaagtaatgataatgataatgcgaattcagtaatcattgaacgaca 323
0Y 61 ttgcgcccgcaglatcttgcgcggagatcctgtttgcgaacgcatcattcaacctcaacg 120
Db 324 ttgcgcccgcaglatcttgcgcggagatcctgttcgagcgatcattcaacctcgaaac 383
0Y 121 c-----ccgggttgggtgttggggaatcggaagccctt-gcggcaagccggcccgaaat 174
Db 384 cctcgagcccccctcggcgttggggaatcggcctccctcctllagcggttgcgcgttcgaaat 443
0Y 175 ctagtgcgcgttcgctgcagcttcacatgcgttagtag-taaaacctcgcaactgtgtac 233
Db 444 acagtgcggtctcgtcgcgaagcctctcctcgcgagtagtcttgcacactcgcatcggagac 503
0Y 234 gcgcgcgcgcga-aagcgtttaaaccacaacttcg-aatgttgacctgcgaatgagtt 291
Db 504 gcgcgcgtctccacagcgtttaaaccacaacttcgaatgttgacctcgcgtcagtagt 563
0Y 292 gaataccgcgttaacttaa 310
Db 564 gaataccgcgttaacttaa 582

RESULT 7
AAVS9007

ID	AAV59007 standard; DNA; 546 BP.
XX	AAV59007;
AC	
XX	
DT	06-JAN-1999 (first entry)
XX	
DE	F. poae Internal transcribed spacer.
XX	
KW	Internal transcribed spacer; ITS; Microdochium; Fusarium; wheat pathogen;
KM	fungal pathogen identification; infection identification; ss.
XX	
OS	Fusarium poae.
XX	
EH	Key Location/Qualifiers
FT	misc_feature 31..160
FT	/*tag= a
FT	/note= "ITS1"
FT	misc_feature 338..489
FT	/*tag= b
FT	/note= "ITS2"
XX	
PN	US5827695-A.
XX	
PD	27-OCT-1998.
XX	
PF	01-AUG-1997; 97US-0905314.
XX	
PR	01-AUG-1997; 97US-0905314.
XX	
PA	(NOVS) NOVARTIS FINANCE CORP.
XX	
PI	Beck JJ;
XX	
DR	WPI: 1998-593995/50.
XX	
PT	Wheat pathogen internal transcribed spacer sequences - used as a
PT	basis for primers for the species-specific polymerase chain reaction
PT	detection of the pathogens
XX	
PS	Claim 1: Column 25-26; 20pp; English.
XX	
CC	This sequence represents an internal transcribed spacer (ITS) sequence of
CC	the invention. The primer pairs, based on the ITS sequences, are used for
CC	the PCR amplification detection of wheat Microdochium and Fusarium fungal
CC	pathogens, especially M. nivale, F. graminearum, F. culmorum,
CC	F. avenaceum, F. poae, F. moniliforme or F. roseum. The two different
CC	strains of fungi show different symptoms during infection, which may or
CC	may not be due to infection. Early identification of the strain causing
CC	the infection allows early, and more specific fungicidal treatment.
XX	
SO	Sequence 546 BP; 150 A; 140 C; 125 G; 131 T; 0 other;

Query Match 60.5%; Score 187.6; DB 19; Length 546;

Best Local Similarity 84.5%; Pred. No. 2,1e-55;

Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4

QY	1	aaatgcataagtaatgtaattgcgaataatcaagtgaatcatcgaaattcttgaagcaca	60
DB	21	aaatgcataagtaatgtaattgcgaatctcagaaattcagtaatcatcgaaattcttgaagcaca	290
QY	61	tttgcccgccgcaagatctctgcggcgatcgctcgttcggagcgatcattcaaccccaagcc	120
DB	291	tttgcccgccgcaagatctctgcggcgatcgctcgttcggagcgatcattcaaccccaagcc	350
QY	121	cccgaggttggtgtctggggatcgcaagcccttgcggcaagccgcccgaatactagt	180
DB	351	c--agcttggtgtggg-----atctgtgtgcaaaacacagctccccaatttgatgt	398
QY	181	ggcgctcgctgcaagcttcattctggttagtgaataaaccttcgcaactggtgaacggcg	240
DB	399	ggcgctcagcgtctgagcttcataagcgttagtgaataaacacatcgtaactggtgaatcg	457

OS	Fusarium culmorum.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..12
FT	/*tag= a
FT	/note= "3' end of small subunit rRNA gene"
FT	13..161
FT	/*tag= b
FT	/note= "ITS 1"
FT	162..318
FT	/*tag= c
FT	/note= "5.8S rRNA gene"
FT	319..472
FT	/*tag= d
FT	/note= "ITS 2"
FT	473..504
FT	/*tag= e
FT	/note= "5' end of large subunit rRNA gene"
XX	
PN	US5814453-A.
PD	29-SEP-1998.
XX	
PF	02-JUL-1997; 97US-0887480.
XX	
PR	02-JUL-1997; 97US-0887480.
PR	19-APR-1995; 95MO-US04712.
PR	15-OCT-1996; 96US-0722187.
XX	
PA	(NOVS) NOVARTIS FINANCE CORP.
XX	
PI	Beck JJ;
XX	
DR	WPI: 1998-541745/46.
XX	
PT	DNA isolated from fungal RNA, and its internal transcribed spacer
XX	sequence - used for detecting fungal pathogens in plant tissue
XX	
PS	Claim 2; Fig 3; 56pp; English.
XX	
CC	This represents the consensus DNA sequence of the internal transcribed
CC	spacer (ITS) region that was PCR amplified from Fusarium culmorum
CC	isolates, R-5106, R-5126 and R-5146. The invention provides a DNA
CC	molecule isolated from the ribosomal RNA (rRNA) gene region of a fungal
CC	pathogen, where the DNA molecule consists of an ITS sequence selected
CC	from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
CC	moniliforme, Septoria avenae or Microdochium nivale. A method for
CC	detecting F. graminearum, F. culmorum, F. moniliforme, F. poae,
CC	F. avenaceum and M. nivale isolates is also provided. The method
CC	comprises isolating DNA from a plant leaf infected with at least one of
CC	the above pathogens and amplifying parts of the ITS sequence of the
CC	pathogen(s) by PCR using specific primers from within these sequences.
CC	The pathogen(s) are detected by visualising the amplified part of the
CC	ITS sequence.
XX	
SO	Sequence 504 BP; 133 A; 132 C; 113 G; 122 T; 4 other:
XX	
Query Match	60.2%; Score 186.6; DB 19; Length 504;
Best Local Similarity	82.6%; Pred. No. 4.6e-55;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;	
DB	1 aaatcgatgaatgaatggaattgcgaataaattgaagatcatcgaattcttgaagcaca 60
DB	212 aaatcgagaagaatgaatggaattgcgaataatcgaatgaatcatcgaattcttgaagcaca 271
QY	61 ttctgcgccgcacgaattctctgcgcgcacatgcctcttgcagcgcgtcatctcaaccctcaagc 120
DB	272 ttgcgcgccgcacgaattctctgcgcgcacatgcctcttgcagcgcgtcatctcaaccctcaagc 331
QY	121 ccgcggtttgtgtgttggggatcgcgaagcccttgcgcgcgcgcgcgcgcgcgcgaattagt 180
DB	332 c---agacttggtgtgtggg999-----agctgaagctcgtgctgacatccccaatacatg 380

QY	181	gcggtctgcgtcgagcttcattcgtagtvgtaaaaccctcgcaactcgtgacggcg	240
DB	381	gcggttcacgtcgragcttcacatagcgtagtaattacatactgctacgtgatactgc	440
OY	241	gcccagccgcttaaaccccccaactctgcatgttctgactcgatcaggttaagaataccg	300
DB	441	ggcgcgcgcgttaaa-cccccaactctgaaigttagcctcgatcaggtagaataccg	499
OY	301	ctgaa 305	
DB	500	ctgaa 504	
RESULT 12			
ID	AAx90111	standard; DNA: 610 BP.	
AC	AAx90111;		
XX	17-SEP-1999	(first entry)	
DE	Phomopsis viticola (variant 2) Internal transcribed spacer DNA sequence.		
XX	ITS1: ITS2: Internal transcribed spacer; detection: fungal pathogen;		
KW	grape; ribosomal RNA gene region; identification: wine; ds.		
XX	Phomopsis viticola.		
OS	MO929899-A1.		
PN	17-JUN-1999.		
XX	07-DEC-1998;	98WO-US25210.	
PF	08-DEC-1997;	97US-0986727.	
PR	(GALL-) GALLO WINERY E & J.		
XX	Descenzo RA, Engel SR, Irelan NA;		
PI	WP1: 1999-429921/36.		
DR	Novel primers targeted to internal transcribed spacer region of		
PT	fungal pathogen ribosomal DNA genes		
XX	Disclosure: Page 32; 43pp; English.		
PS	The present invention describes oligonucleotides (I) for identifying		
CC	fungal pathogens, especially of grape plants. The oligonucleotides		
CC	are isolated double stranded nucleic acids representing the internal		
CC	transcribed spacer (ITS) 1 and 2 of ribosomal RNA genes from the		
CC	organisms Eutypella vitis, Eutypa lata, Phomopsis viticola or		
CC	Diplodia gossypina. The oligonucleotide are used to detect the fungal		
CC	pathogens Eutypella vitis, Eutypa lata, Phomopsis viticola or Diplodia		
CC	gossypina, especially when infecting grape plants. The detection method		
CC	is used in the wine industry. AAX90075 to AAX90094 represent		
CC	specifically claimed oligonucleotides from the present invention.		
CC	AAX90095 to AAX90105 represent specifically claimed PCR primers for use		
CC	in the detection of the fungal pathogens Eutypella vitis, Eutypa lata,		
CC	Phomopsis viticola or Diplodia gossypina. The present sequence represents		
CC	an ITS DNA sequence from the present invention.		
XX			
SO	Sequence 610 BP; 150 A; 175 C; 163 G; 122 T; 0 other;		
Query Match 59.7%; Score 185; DB 20; Length 610;			
Best Local Similarity 83.1%; Pred. No. 1.8e-54;			
Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;			
OY	1	aaatgcgataagtaactgtaattgcacaaatccagtgaaatcatcgaattcttgaacgcaca	60
DB	283	aaatgcgataagtaactgtaattgcagaaatccagtgaaatcatcgaattcttgaacgcaca	342

XX	Sequence	545 bp; 148 A; 143 C; 125 G; 129 T; 0 other:
SO	Query Match	59.1%; Score 183.2; DB 19; Length 545;
	Best Local Similarity	83.5%; Pred. No. 7.3e-54;
	Matches 259; Conservative	0; Mismatches 38; Indels 13; Gaps 4;
QY	1 aatcgcataagtaattgtgaattgcgaataatccagtgaaatcatcatgattttggaagcaca	60
DB	229 aatcgcataagtaattgtgaattgcgaataatccagtgaaatcatcatgattttggaagcaca	288
QY	61 ttgcgcgccgcagatattctgcggcgacatgcctggttcggagcgatcatcctaaccctaagcc	120
DB	289 ttgcgcgccgcagatattctgcggcgacatgcctggttcggagcgatcatcctaaccctaagcc	348
QY	121 cccggagtttgtgtgttgaggatcggcaagcccttcgscgaagccggccccaatctagtg	180
DB	349 c---agcttgtgtgttgaggatcggcaagcccttcgscgaagccggccccaatctagtg	397
QY	181 ggggagctgcgtcgaacttcgaattcgtgtagtaaaacccctgcgaactcgtgacggcggc	240
DB	398 ggggagctgcgtcgaacttcgaattcgtgtagtaaaacccctgcgaactcgtgacggcggc	456
QY	241 ggcgcacgcgttaaaccccccaacttcgaaatgttgcacctgcgatacaggtaagaataccgc	300
DB	457 ggcgcacgcgttaaac---cccccaacttcgaaatgttgcacctgcgatacaggtaagaataccgc	515
QY	301 ctgaacttaa 310	
DB	516 ctgaacttaa 525	
RESULT 14		
AAV62593		
ID	AAV62593 standard; DNA; 545 bp.	
XX	AAV62593;	
AC		
XX		
DT	17-DEC-1998 (first entry)	
XX		
DE	Fusarium moniliforme PCR amplified ITS region DNA sequence.	
XX		
KW	Internal transcribed spacer; ITS; ribosomal RNA; rRNA; fungal pathogen;	
KW	Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;	
KW	Seפורית avenae; Microdochium nivale; Fusarium poae; Fusarium avenaceum;	
KW	PCR; nucleic acid detection; ss.	
XX		
OS	Fusarium moniliforme.	
XX		
EH	Key	Location/Qualifiers
FT	misc_feature	1..30
FT		/tag= a
FT		/note= "3' end of small subunit rRNA gene"
FT	misc_feature	31..178
FT		/tag= b
FT		/note= "ITS 1"
FT	misc_feature	179..335
FT		/tag= c
FT		/note= "5.8S rRNA gene"
FT	misc_feature	336..488
FT		/tag= d
FT		/note= "ITS 2"
FT	misc_feature	489..545
FT		/tag= e
FT		/note= "5' end of large subunit rRNA gene"
XX		
PN	US5814453-A.	
XX		
PD	29-SEP-1998.	
XX		
PE	02-JUL-1997; 97US-0887480.	
XX		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:09 ; Search time 5019.06 Seconds
(without alignments)
833.633 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 310
Sequence: 1 aaatgcgataagtaagtga.....ggaataccgcgtgaactaa 310Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estt:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109.2	35.2	214	10	BF251183 EST418443
2	100.8	32.5	213	9	A1209736 c7908a1.f
3	100.8	32.5	318	9	A1213025 y6f01a1.f
4	97.6	31.5	846	12	CNS07820 AL434652 T7 end of
5	97.6	31.5	893	12	CNS07820 AL435182 T7 end of
6	97.6	31.5	995	12	CNS07820 AL435966 T7 end of
7	97.6	31.5	999	12	CNS07820 AL432204 T7 end of
8	97.6	31.5	1034	12	CNS07820 AL435957 T7 end of
9	97.6	31.5	1094	12	CNS07820 AL431760 T7 end of
10	97.6	31.5	1098	12	CNS07820 AL433404 T3 end of
11	97.2	31.4	981	12	CNS07820 AL431115 T7 end of
12	96.4	31.1	525	12	A2927454 AL432204 T7 end of
13	96.4	31.1	522	12	A2927454 AL432204 T7 end of
14	96.2	31.0	870	12	CNS06K29 AL403531 T7 end of
15	96.2	31.0	1004	12	CNS06K29 AL402853 T3 end of
16	96.2	31.0	1043	12	CNS06K29 AL404672 T7 end of
17	96	31.0	638	10	BE337372 BE337372 894045B04

18	96	31.0	969	12	CNS07DPM AL439868 T7 end of
19	96	31.0	971	12	CNS07DPL AL440767 T3 end of
20	96	31.0	982	12	CNS07D5J AL440045 T3 end of
21	96	31.0	994	12	CNS07CUT AL439664 T3 end of
22	96	31.0	1014	12	CNS07CUT AL439205 T7 end of
23	96	31.0	1027	12	CNS07DYS AL441098 T3 end of
24	96	31.0	1042	12	CNS07CH2 AL443919 T3 end of
25	96	31.0	1052	12	CNS07DPT AL440775 T3 end of
26	96	31.0	1110	12	CNS07EB9 AL441547 T3 end of
27	95.6	30.8	1010	12	CNS07C1H AL438603 T7 end of
28	95.6	30.8	1029	12	CNS07AHC AL436582 T7 end of
29	95.4	30.8	939	12	CNS06KH6 AL440288 T7 end of
30	94.8	30.6	440	12	A2931033 AL42931033 474.dhz61
31	94.8	30.6	480	12	A2931805 AL42931805 474.dhz62
32	94.8	30.6	503	12	A2931107 AL42931107 474.dhz62
33	94.8	30.6	508	12	A2930634 AL42930634 474.dhz62
34	94.8	30.6	518	12	A2930375 AL42930375 474.dhz62
35	94.4	30.5	1009	12	CNS07DE3 AL440353 T3 end of
36	93.8	30.3	1025	12	CNS06XGS AL4419714 T3 end of
37	93.6	30.2	1037	12	CNS06OXE AL408648 T7 end of
38	93.4	30.1	900	12	CNS06ZCK AL422298 T7 end of
39	93.4	30.1	929	12	CNS06UDM AL416190 T7 end of
40	93	30.0	675	12	CNS06Y1Q AL421080 T7 end of
41	93	30.0	725	12	CNS06XRL AL420083 T3 end of
42	93	30.0	823	12	CNS06Y58 AL420594 T3 end of
43	93	30.0	867	12	CNS06Z9V AL422057 T3 end of
44	93	30.0	879	12	CNS06Y5H AL420603 T7 end of
45	93	30.0	896	12	CNS06YXF AL421609 T7 end of

ALIGNMENTS

RESULT 1
BF251183
LOCUS EST418443
DEFINITION Coccioidioides immitis spherule cDNA library Coccioidioides immitis cDNA clone CIAAD94 5' sequence, mRNA sequence.
ACCESSION BF251183
VERSION BF251183.1 GI:16931326
KEYWORDS EST.
SOURCE Coccioidioides immitis.
ORGANISM Coccioidioides immitis.
REFERENCE 1 (bases 1 to 214)
AUTHORS Gardner,M.J. and Kirkland,T.
TITLE Generation of ESTs from Coccioidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source location/Qualifiers
1..214
/organism="Coccioidioides immitis"
/db_xref="taxon:5501"
/clone="CIAAD94"
/clone.lib="Coccioidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 46 a 54 c 62 g 52 t
ORIGIN

Query Match 35.2%; Score 109.2; DB 10; Length 214;
Best Local Similarity 78.3%; Pred. No. 9.3e-23;
Matches 144; Conservative 0; Mismatches 38; Indels 2; Gaps 1;

Oy	1	aaatgcgataagtaatgtgaatgtgaaatcaaggaatcagaaatctttgaacgcaca	60
Db	14	AAATCGCATAACTAATGTGAATTGCAGAAATTCGTAATCATCGAATCTTTGAAAGCACA	73
Oy	61	ttgcgcgcgcgcagtaattcttgcgcgcgcacatgcttctcgagcgcgtcatctcaacctcaagcc	120
Db	74	TTGCGCCCTCTGTGATTTTCCGGGGGCATTCGCTGTTGAGACGTCATTGGCAAAOCCCTTTCAG	133
Oy	121	cccgagtttggttglttgcgggagatcgcgaagcccttgcgcgaagccgcgcacccaatctagtg	180
Db	134	CACGCGCTTGTGTGTGGGCCAAACCTCCCGCGCTTGTG--TGACGCGGGCCTGAATGATCAGTG	191
Oy	181	gcgag 184	
Db	192	gcgg 195	

	RESULT	2
Locus	A1209736/c	
Definition	c7g08a1.f1 Aspergillus nidulans 24hr asesexual developmental and vegetative cDNA lambda zap library Emericella nidulans CDNA clone c7g08a1.3', mRNA sequence.	
Accession	A1209736	
Version	A1209736	
Keywords	EST.	
Source	A1209736.1 GI:3771678	
Organism	Emericella nidulans. Emericella nidulans Eurotiota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella. 1 (bases 1 to 213) Klipfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B. An Aspergillus nidulans EST Database Unpublished (1998) Other-ESTs: c7g08a1.r1 Contact: Bruce A. Roe, University of Oklahoma, broeou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel.: 405 325 4912 Fax: 405 325 7762 Email: broeou.edu We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center. Seq primer: M13-20.	213 bp mRNA linear EST 19-OCT-1998

FEATURES	SOURCE	Location/Qualifiers
	1. .213	/organism="Emmericella nidulans" /strain="FGSC A26" /db_xref="taxon:162425" /clone="c7g08a1" /clone_11b="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library" /tissue_type="vegetative mycelia asexual structures" /note="Vector: pBluescript SK+ Site1: EcoRI; Site2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT	43 a	68 c 63 g 39 t
ORIGIN		

Query Match	32.5%	Score 100.8	DB: 9	Length 213
Best Local Similarity	74.5%	Prod. No. 3.3e-20		
Matches 155:	Conservative	0	Mismatches 47	Indels 6
			Gaps	2

OY	1	aatgcgataagtaatcgtgaattgcacaatcagtcgatcatcgaatccttgaagccaca	60
Db	202	AACGCGATAGTAAATGTGAATTCGCAATCATCTGATCATTCAGCTTTGAACGCACA	143
OY	61	ttggccgccgaagatcttcggcggaatgcctgttcgaagcgtcaatccaacctcaagcc	120

Db 142 TTGGGCCCCCTGGGCAATCCGGGGGGGAGCATCCCTGCTCCGAGCCTCATCTGCTGGCCCTCAAG -- 83
Oy 121 CCCGGGTGTTGTTGTTGGGATCGCAAGGCCCTTGGGCAAGCCGCCCCGGAATCTAGT 180
Db 84 CCGGGCTTGATGTCTTGGGTGTCGTCGCCCCCGGGG----GACGGGCCCGAAGGACGCG 29
Oy 181 ggagcttcgcgtcagcttccattcgta 208
Db 28 GCGGACCGGTGCTCGGCTCTCGAGCTA 1

RESULT	3				
LOCUS	AI213025/c				
DEFINITION		318 bp	mRNA	linear	EST 19-OCT-1996
	y6f01a1.r1	<i>Aspergillus nidulans</i> 24hr asexual developmental and			
	vegetative cDNA lambda zap library	<i>Emmericella nidulans</i> cDNA clone			
	y6f01a1 3', mRNA sequence.				
ACCESSION	AI213025				
VERSION	AI213025.1	GI:3774967			
KEYWORDS	EST.				
SOURCE	<i>Emmericella nidulans</i> .				
ORGANISM	<i>Emmericella nidulans</i>				
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				
	Eurotiiales; Trichocomaceae; <i>Emmericella</i> .				
REFERENCE	1 (bases 1 to 318)				
AUTHORS	Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,				
	Prade, R., and Roe, B.				
	An <i>Aspergillus nidulans</i> EST Database				
	Unpublished (1998)				
TITLE	Other_ESTs: y6f01a1.r1				
JOURNAL	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu				
COMMENT	Department of Chemistry and Biochemistry				
	Advanced Center for Genome Technology, University of Oklahoma				
	620 Parrington Oval, Norman, OK 73019, USA				
	Tel: 405 325 4912				
	Fax: 405 325 7762				
	Email: broe@ou.edu				
	We anticipate the future release of the cDNA clones to the Fungal				
	Genetics Stock Center				
	Seq primer: M13-20				
	High quality sequence stop: 265.				

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FEATURES
    source
        location/Qualifiers
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                /organism="Emmericella nidulans"
                /strain="EGSC A26"
                /db_xref="taxon:162425"
                /clone="y6f01a1"
                /clone_11b="Aspergillus nidulans 24hr asexual
                developmental and vegetative cDNA lambda zap library"
                /tissue.type="vegetative mycelia, axonal structures"
                /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
                3' end of cDNA cloned into XhoI site of pBluescript"
        69 a 93 c 88 g 68 t

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Query Match	32.5%	Score 100.8	DB 9	Length 318
Best Local Similarity	74.5%	Pred. No. 4e-20		
Matches 155	Conservative 0	Mismatches 47	Indels 6	Gaps 2

QY	1	aatgcatgaatgaatgcaattgcgaataatcagtcagatcatcgaatccttgaagcaca	60
Db	204	AACGTGGATTAAGTAATGTGAATTGCAGAAATTCAGTAATCATGAGCTTTGAACCCANA	145
QY	61	ttgcgcgcgcgcgaattcttgcgggcgcatgcctgttgcagtcatttcaacctcaagcc	120
Db	144	TTGCGCCCTTCGTGGCAATTCGGGGGGCAAGCTTGCCACAGCGTATTGTCGCCCTCAAG--	85
QY	121	cccgaggtttgtgtcttgcgggacgcgaagccttgcgcgaagccgcgcgcgaatctcagtg	180
Db	86	CCCGGCTTGTGTGTTGGGTGCTGCTGCCCCCGGG---GACGGGGCCGGAAGGCGAGCG	31

Db	30	CGGACACCGTGTCCGGTCTCTCGAGCGTA	3
RESULT	4		
CNS07820		846 bp	DNA
LOCUS		77 end of clone BB0AA025B03 of library BB0AA from strain CBS 4732	linear GSS 08-JUL-2001
DEFINITION			
ACCESSION		AL434652	
VERSION		AL434652.1	GI:12218066
KEYWORDS		GSS.	
SOURCE		<i>Pichia angusta</i> .	
ORGANISM		<i>Pichia angusta</i> .	
REFERENCE		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.	
AUTHORS		1 (bases 1 to 846)	
TITLE		Blandin,G., Florente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.	
JOURNAL		Genomic exploration of the hemiascomycetous yeasts: 13. <i>Pichia angusta</i>	
MEDLINE		FEBS Lett. 487 (1), 76-81 (2000)	
REFERENCE		2 (bases 1 to 846)	
AUTHORS		Souciat,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boitlin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Florente,B., Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S., Saurin,W., Yekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.	
TITLE		Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies	
JOURNAL		FEBS Lett. 487 (1), 3-12 (2000)	
MEDLINE		20584711	
REFERENCE		3 (bases 1 to 846)	
AUTHORS		Genoscope.	
TITLE		Direct Submission	
JOURNAL		Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : sequefr@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT		This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvatum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.	
FEATURES		Location/Qualifiers	
SOURCE		1..846	
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		/strain="CBS 4732"	
		/db_xref="taxon:4905"	
		/clone="BB0AA025B03"	
		/clone_1lb="BB0AA"	
		/note="end : 77"	
		<1..>846	
		/note="Part of rDNA repeats contains 35S rDNA"	
		/evidence="not experimental"	
BASE COUNT	224 a	165 c	188 g
ORIGIN		267 t	2 others
Query Match	31.5%	Score 97.6;	DB 12; Length 846;
Best Local Similarity	85.7%	Pred. No. 5.8e-19;	
Matches 120; Conservative	0;	Mismatches 19;	Indels 1; Gaps 1;
1	aaagcgataagtaatcgtgaattccaataatcagtcgaatcatcgaaattcttgaacgcaca	60	

Oy	61	ttgcgcccgccagatcttcggcgggcatgcctgttgcaggcatcttcaaccctccaagcc	120
Db	522	ttggccccccttgatttccagagggcagtgcctgtttgagcggtcatatttc-cctctcaaac	580
Oy	121	ccccgggttgtgtcttgggga	140
Db	581	ctcggggtttggtgatgggca	600

RESULT 5
CNS079EG 893 bp DNA linear GSS 08-JUL-2001
LOCUS t7 end of clone BB0AA028D03 of library BB0AA from strain CBS 4732
DEFINITION Pichia angusta, genomic survey sequence.
ACCESSION AL435182
VERSION AL435182 GI:12218595
KEYWORDS GSS.
SOURCE Pichia angusta.
ORGANISM Pichia angusta.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
REFERENCE 1 (bases 1 to 893)
Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
angusta
FEBS Lett. 487 (1), 76-81 (2000)
JOURNAL MEDLINE 20584723
REFERENCE 2 (bases 1 to 893)
Souci t,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Mesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
JOURNAL MEDLINE 20584711
REFERENCE 3 (bases 1 to 893)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Séquencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Hansenula lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source
Location/Qualifiers
1..893
/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA028D03"
/clone_id="BB0AA"
/note="end : 77"
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/note="part of rDNA repeats
contains 35S rDNA"
/evidence=not_experimental

BASE COUNT 244 a 160 c 226 g 261 t 2 others
ORIGIN

/db_xref="taxon:4905"
/clone="BB0A009A07"
/clone_lib="BB0A"
/note="end : T7"
<1..>999
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"
BASE COUNT 237 a 212 c 235 g 313 t 2 others
ORIGIN

Query Match 31.5%; Score 97.6; DB 12; Length 999;
Best Local Similarity 85.7%; Pred. No. 6.3e-19;
Matches 120; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

OY 1 aatgcgataagtaatgtaattgcaaaattcagtcgaatcgcgaatcttgaacgaca 60
DB 718 AAATGCGATACGTAATGTAATGCAATTTGTCGTAATCATTTGAACGCACA 777
OY 61 ttgcgcgcgcagatcttcgagcgagcctgctgctgagcgcattcaaccctaaagcc 120
DB 778 TTGCGCCCTCTGTGATTCCAGAGGCGCATCCGTGTTGACGTCATTTTC-CCTCTCAAAC 836
OY 121 cccgggttggtggtgggga 140
DB 837 CTCGGGTTGGTGATGCGCA 856

RESULT 8
LOCUS CNS0792Z 1034 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone XBB0A002E02 of library XBB0A from strain CBS 4732
ACCESSION AL435957
VERSION AL435957
KEYWORDS
SOURCE GSS
ORGANISM *Pichia angusta*.

REFERENCE 1 (bases 1 to 1034)
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia*

TITLE *angusta*
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
REFERENCE 2 (bases 1 to 1034)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 1034)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
MEDLINE 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
REFERENCE segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
AUTHORS This GSS is part of a random genomic sequencing program of thirteen
JOURNAL yeast species: *Saccharomyces bayanus* var. *uvorum*, *Saccharomyces*
TITLE *exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
AUTHORS *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces*
COMMENT *lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Tarowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of
the other extremity of this insert.
Location/Qualifiers
1..1034
/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0A002E02"
/clone_lib="BB0A"
/note="end : T7"
<1..>1034
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not_experimental"
BASE COUNT 320 a 241 c 208 g 263 t 2 others
ORIGIN

misc-feature

Query Match 31.5%; Score 97.6; DB 12; Length 1034;
Best Local Similarity 85.7%; Pred. No. 6.4e-19;
Matches 120; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

OY 1 aatgcgataagtaatgtaattgcaaaattcagtcgaatcgcgaatcttgaacgaca 60
DB 498 AAATGCGATACGTAATGTAATGCAATTTGTCGTAATCATTTGAACGCACA 439
OY 61 ttgcgcgcgcagatcttcgagcgagcctgctgctgagcgcattcaaccctaaagcc 120
DB 438 TTGCGCCCTCTGTGATTCCAGAGGCGCATCCGTGTTGACGTCATTTTC-CCTCTCAAAC 380
OY 121 cccgggttggtggtgggga 140
DB 379 CTCGGGTTGGTGATGCGCA 360

RESULT 9
LOCUS CNS076RE 1094 bp DNA linear GSS 08-JUL-2001
DEFINITION T7 end of clone BB0A006D05 of library BB0A from strain CBS 4732
ACCESSION AL431760
VERSION AL431760
KEYWORDS
SOURCE GSS
ORGANISM *Pichia angusta*.

REFERENCE 1 (bases 1 to 1094)
AUTHORS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; *Pichia*.

TITLE Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia*
angusta
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
REFERENCE 2 (bases 1 to 1094)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 1094)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
MEDLINE 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
REFERENCE segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
AUTHORS This GSS is part of a random genomic sequencing program of thirteen
JOURNAL yeast species: *Saccharomyces bayanus* var. *uvorum*, *Saccharomyces*
COMMENT *exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Tarowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See

exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

Location/Qualifiers
1..1094

/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA006005"
/clone_lib="BB0AA"
/note="end : T3"
misc_feature
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not experimental"

BASE COUNT 336 a 269 c 192 g 293 t 4 others
ORIGIN

Query Match 31.5%; Score 97.6; DB 12; Length 1094;
Best Local Similarity 85.7%; Pred. No. 6.5e-19;
Matches 120; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

OY 1 aatgcgataagtaatgtaattgcaaaatcagtaatcattcgaacgcaca 60
||||| ||||||| ||||||| || ||||||| ||||||| ||||||| |||||||
DB 819 AATGCGATACGTAATGTAATTCGATTCGATTCATGTAATTCGTAACGCACA 760
OY 61 ttggcccccgcagatcttgcgcgcagtcgttcgagcgatcattcaaccctaacgc 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 759 TTGCGCCCTCTGTGTAATTCAGAGGCGATGCTGTTGAGCGTCAATTC-CCTCTCAAAACC 701
OY 121 cccgggttgggtgtgtgggga 140
||||| ||||||| |||||
DB 700 CTCGGGTTGTGTGATGGCA 681

RESULT 10 1098 bp DNA linear GSS 08-JUL-2001
LOCUS CDS07812/c
DEFINITION T3 end of clone BB0AA017B06 of library BB0AA from strain CBS 4732
ACCESSION AL433404
VERSION AL433404.1 GI:12216818
KEYWORDS GSS.
SOURCE Pichia angusta.
ORGANISM Pichia angusta.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 1098)
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
TITLE Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
angusta
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
REFERENCE 2 (bases 1 to 1098)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boloiti-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekaita,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
REFERENCE 3 (bases 1 to 1098)
AUTHORS Genoscope.

TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: *Saccharomyces bayanus* var. *uvorum*, *Saccharomyces*
exiguus, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES

source

Location/Qualifiers
1..1098

/organism="Pichia angusta"
/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA017B06"
/clone_lib="BB0AA"
/note="end : T3"
misc_feature
/note="part of rDNA repeats
contains 35S rDNA"
/evidence="not experimental"

BASE COUNT 338 a 268 c 193 g 298 t 1 others
ORIGIN

Query Match 31.5%; Score 97.6; DB 12; Length 1098;
Best Local Similarity 85.7%; Pred. No. 6.5e-19;
Matches 120; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

OY 1 aatgcgataagtaatgtaattgcaaaatcagtaatcattcgaacgcaca 60
||||| ||||||| ||||||| || ||||||| ||||||| ||||||| |||||||
DB 827 AATGCGATACGTAATGTAATTCGATTCGATTCATGTAATTCGTAACGCACA 768
OY 61 ttggcccccgcagatcttgcgcgcagtcgttcgagcgatcattcaaccctaacgc 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 767 TTGCGCCCTCTGTGTAATTCAGAGGCGATGCTGTTGAGCGTCAATTC-CCTCTCAAAACC 709
OY 121 cccgggttgggtgtgtgggga 140
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DB 708 CTCGGGTTGTGTGATGGCA 689

RESULT 11 981 bp DNA linear GSS 07-JUL-2001
LOCUS CDS0769H/c
DEFINITION T7 end of clone BB0AA002A09 of library BB0AA from strain CBS 4732
ACCESSION AL431115
VERSION AL431115.1 GI:12214527
KEYWORDS GSS.
SOURCE Pichia angusta.
ORGANISM Pichia angusta.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE 1 (bases 1 to 981)
AUTHORS Blandin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
and Dujon,B.
TITLE Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
angusta
JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
MEDLINE 20584723
REFERENCE 2 (bases 1 to 981)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boloiti-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekaita,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.

Query Match Similarity 31.1% Score 96.4 DB 12 Length 522:
Best Local Similarity 81.2% Pred. Nsm 1.1e-18;
Matches 112; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy 1 aaatgcataagtaabtgaaattgcaaaaattgaatgaatcatcagaactcttgaacgaca 60
|||||
Db 403 AATGCGAGTACGTAAATGTAATTGGCAATTCCTGGAATCATGCAGATCTTTGAGCACA 344
|||||

Oy 61 ttggcgccgccgatcttcggcgsgcatgcctgttcgagcgatcattcaacctcaagcc 120
||||| | |||||
Db 343 TTGCGCCCTTGCTGTATTCAGAGGGGCAATCCGTGTTGACGCCATTTCTTCAAAAGA 284
||||| | ||||| | ||

Oy 121 cccgagtttggtgtgag 138
| | ||||| | |
Db 283 CTTCTTGTGTGATGAG 266

RESULT 14
CONS06K29 870 bp DNA linear GSS 17-JUN-2001
LOCUS T7 end of clone AT0AA009C05 of library AT0AA from strain CBS 4311
DEFINITION Of Saccharomyces servazzii, genomic survey sequence.
ACCESSION ALA03531
VERSION ALA03531.1 GI:12163884
KEYWORDS GSS.
SOURCE Saccharomyces servazzii.
ORGANISM Saccharomyces servazzii.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
1 (bases 1 to 870)
Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H.,
Artiguenave,F., Wincker,P. and Galliardin,C.
Genomic exploration of the hemiascomycetous yeasts : 7.
Saccharomyces servazzii
FEBS Lett. 487 (1), 47-51 (2000)

JOURNAL MEDLINE
REFERENCE 20584717
AUTHORS 2 (bases 1 to 870)
Souciet,J.L., Algle,M., Artiguenave,F., Blandin,G.,
Boloitin-Puknara,M., Bon,E., Brochier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durand,P., Lepingle,A., Llorente,B.,
Maupertuy,A., Neuveglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nioche,C., Mesosclowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts : 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL MEDLINE
REFERENCE 20584711
AUTHORS 3 (bases 1 to 870)
Genoscope.
Direct Submision
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seque@genoscope.cns.fr Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
SOURCE location/Qualifiers
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/organism="Saccharomyces servazzii"
/strain="CBS 4311"
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/clone="AT0AA009C05"
/clone_1kb="AT0AA"
/note="end : T7"
<1.. >870
/note="part of rDNA repeats"

misc_feature

BASE COUNT	214 a	177 c	214 g	260 t	5 others
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Best Local Similarity	80.1%; Pred. No. 1.6e-18;				
Matches 113; Conservative	0; Mismatches 28; Indels 0; Gaps 0;				
Qy	1 aatgagataagtaatgtaattgtaattgcaaaaattcaatgtaatcatcatgtaatttgaacgcaca 60				
Db	575 AATATGGAATACATTAATGTAATTTGAGATTCCTGCAATCATCATCATCTTTTGAAACGCACA 634				
Qy	61 ttgcgcgccgcacgaattctgcgcggcagcgcctgtctgcagcgcgcattcaaccctcaagcc 120				
Db	635 TTGCGCGCCCTCTGTGTATTCACAGGGCGATGCCCTTTGACGCGTCATTCTTTCTCAAAACG 694				
Qy	121 cccgagtttgtgtgtgggagat 141				
Db	695 CAATGTTTGCTGTGTGAGTGAT 715				
RESULT 15					
CNS06KGF					
LOCUS	CNS06KGF 1004 bp DNA linear GSS 17-JUN-2001				
DEFINITION	T3 end of clone AT0AA005B03 of library AT0AA from strain CBS 4311				
ACCESSION	AL0402853				
VERSION	AL0402853.1 GI:12162391				
KEYWORDS	GSS.				
SOURCE	Saccharomyces servazzii.				
ORGANISM	Saccharomyces servazzii.				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
AUTHORS	Saccharomycetales; Saccharomycetaceae; Saccharomyces.				
TITLE	1 (bases 1 to 1004)				
JOURNAL	Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H.,				
MEDLINE	Artiguenave,F., Wincker,P. and Galliard,C. 7.				
REFERENCE	Genomic exploration of the hemiascomycetous yeasts: 7.				
AUTHORS	FEMS Lett. 487 (1), 47-51 (2000)				
TITLE	2 (bases 1 to 1004)				
JOURNAL	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,				
MEDLINE	Bojotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,				
AUTHORS	de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B.,				
TITLE	Malpertuy,A., Neuveglise,C., Ozler-Kalogeropoulos,O., Potier,S.,				
JOURNAL	Saurin,M., Texala,F., Toffano-Nicche,C., Wesolowski-Louvel,M.,				
MEDLINE	Wincker,P. and Weissenbach,J.				
AUTHORS	Genomic exploration of the hemiascomycetous yeasts: 1. A set of				
TITLE	yeast species for molecular evolution studies				
JOURNAL	FEMS Lett. 487 (1), 3-12 (2000)				
MEDLINE	20584711				
AUTHORS	3 (bases 1 to 1004)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
MEDLINE	Submitted (07-SEP-2000) Genoscope - Centre National de Sequenage,				
AUTHORS	2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :				
TITLE	sege@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
JOURNAL	This GSS is part of a random genomic sequencing program of thirteen				
MEDLINE	yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces				
AUTHORS	exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,				
TITLE	Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces				
JOURNAL	lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia				
MEDLINE	anagusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,				
AUTHORS	Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to				
TITLE	5 kb were prepared and both extremities were sequenced. See				
JOURNAL	keywords for description of this sequence and for the sequence of				

RESULT 2
US-08-905-314A-24
Sequence 24, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: STRAIN: Fusarium avenaceum
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..181
OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note="5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..504
OTHER INFORMATION: /note="ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 505..561
OTHER INFORMATION: /note="5' end of large subunit
OTHER INFORMATION: rRNA gene"
US-08-905-314A-24

Query Match 80.6%; Score 249.8; DB 1; Length 561;
Best Local Similarity 91.6%; Pred. No. 3.2e-72;
Matches 285; Conservative 1; Mismatches 23; Indels 2; Gaps 2;
Oy 1 aaatgcataagtaatgtgaatgcataatcagtgaaatccttgaaagcaca 60

DB 232 AAATGCGATAGTAATGTAATGCAGAAATTCAGTGAATCATGCAATCTTGAACGCACA 291
Oy 61 ttgcgcccgcagtaattctggcggaatgcctgttcgaagcatttcaaccctaaagcc 120
DB 292 TTGCGCCCGCTGTAATTCGCGGGCATGCTGTTCGAGGCTCATTTCAACCTCAAGCC 351
Oy 121 cccggtttgtgtgggaatcggaagcccttcgagc-aagccggcccaaatctagt 179
DB 352 CCCGGTTGTGTTGGGATGCGCTGTGCTTMYGGCGGTGCCGCCCGCAATACATT 411
Oy 180 ggcgctcgtcgtcagcttcacatcgtcgtagtaaaaaacctcgcaactgtaacggcg 229
DB 412 GCGCGTCTCGCTGCACGCTCATTTGCGAGTAACTAAGCTGCAACTGGAACGCGCGC 471
Oy 240 cggcagcgcgttaaaccccaacttcgaaatgtttgaccccgatcgaagtaggaataacc 299
DB 472 CGGCGATCCG-TAAACCCCACTTGAATGTTGACCTCGATGAGTAGAATACCC 530
Oy 300 gctgaactaa 310
DB 531 GCTGAACCTAA 541

RESULT 3
US-08-652-127C-8
Sequence 8, Application US/08652127C
Patent No. 5792611
GENERAL INFORMATION:
APPLICANT: Richard C. Hamelin
TITLE OF INVENTION: DETECTION OF PLANT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: George A. Seaby
STREET: 880 Wellington Street, Suite 708
CITY: Ottawa
COUNTRY: Canada
ZIP: K1R 6K7
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,127C
FILING DATE: May 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George A. Seaby
REGISTRATION NUMBER: 24,034
REFERENCE/DOCKET NUMBER: 1898
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 232-5815
TELEFAX: (613) 232-5831
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 583
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-652-127C-8

Query Match 74.5%; Score 231; DB 1; Length 583;
Best Local Similarity 90.4%; Pred. No. 4.4e-66;
Matches 281; Conservative 0; Mismatches 25; Indels 5; Gaps 3;
Oy 1 aaatgcataagtaatgtgaatgcataatcagtgaaatccttgaaagcaca 60
DB 257 AAATGCGATAGTAATGTAATGCAGAAATTCAGTGAATCATGCAATCTTGAACGCACA 316

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OY 61 ttggccggccagatattctggcgggcaatgcctgttcgagcgtcatcttcaaccctcaagcc 120
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 317 ttggccggccagatattctggcggcgcacgctgttcgagcgtcatcttcaaccctcaagcc 376
OY 121 ccggggttgggtgttgggagcagcgaaccccttgcggaacccggcccggaatctagt 180
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 377 cccggcggttggtgttggtgggatcgccgaacctccgcg -gcggccgctcccttcaatctagt 435
OY 181 gcggtctgcgtcagcttcacatgtagtagtaaaacccctcgcaactgtagcgcgagc 240
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 436 cggcgctgcgtgtagcttctcctcgtgtagcagacacctccg -actgggaaacacagcg 492
OY 241 ggcgaagcgttaaaccccgcaacttgaatg-tgaacctgtagtaggtaggaatccc 299
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 493 ggcacacgctttaaaccgcccaacttctgaagattgacgtcgatgagtaagaaatccc 552
OY 300 gctgaactaa 310
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 553 gctgaacttaa 563
```

```
RESULT 4
US-08-652-127C-7
; Sequence 7, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-7
```

```
Query Match 72.6%; Score 225.2; DB 1; Length 531;
Best Local Similarity 86.8%; Pred. No. 3.3e-64;
Matches 277; Conservative 0; Mismatches 30; Indels 5; Gaps 3;
```

```
OY 1 aaatgcgataagtaatgtaattgcaaaatcgaatcgaatcattgaacgcaca 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 203 AAATGCGATAGTAATGTAATGCAAGATTCAGTGAATCAATCTTTGAACGCACA 262
OY 61 ttggccggccagatattctggcgggcaatgcctgttcgagcgtcatcttcaaccctcaagcc 120
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 263 ttggccggccagatattctggcggcgcacgctgttcgagcgtcatcttcaaccctcaagcc 322
```

```
OY 121 ccggggttgggtgttgggagcagcaag-cccttgcggaacccggcccggaatctagt 179
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 323 cccggcggttggtgttgagatngcgtgcccccggcgccgcnmctcttcaatatagt 382
OY 180 ggggtctgcgtcgaacttcacatgtagtagtaaaacccctcgcaactgtagcgagc 239
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 383 GGGGgtctgcgttacttctcctgctgtagtagcagacctccg -actggaaacacagcg 439
OY 240 cggcgaagcgttaaaccccgcaactctg-aatgttgaacctcgatcgaatgtaggaatcc 298
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 440 GGGCAGACCGGTAAACCCGCCACTTCTGAAGAGTTGACTCGATGAGTAATACC 499
OY 299 cgcctgaactaa 310
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 500 CGCTGAACCTTAA 511
```

```
RESULT 5
US-08-652-127C-6
; Sequence 6, Application US/08652127C
; Patent No. 5792611
; GENERAL INFORMATION:
; APPLICANT: Richard C. Hamelin
; TITLE OF INVENTION: DETECTION OF PLANT
; TITLE OF INVENTION: PATHOGEN FUNGI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George A. Seaby
; STREET: 880 Wellington Street, Suite 708
; CITY: Ottawa
; COUNTRY: Canada
; ZIP: K1R 6K7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,127C
; FILING DATE: May 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George A. Seaby
; REGISTRATION NUMBER: 24,034
; REFERENCE/DOCKET NUMBER: 1898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 232-5815
; TELEFAX: (613) 232-5831
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-652-127C-6
```

```
Query Match 72.3%; Score 224.2; DB 1; Length 581;
Best Local Similarity 88.5%; Pred. No. 7.1e-64;
Matches 276; Conservative 1; Mismatches 30; Indels 5; Gaps 3;
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OY 1 aaatgcgataagtaatgtaattgcaaaatcgaatcgaatcattgaacgcaca 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 253 AAATGCGATAGTAATGTAATGCAAGATTCAGTGAATCAATCTTTGAACGCACA 312
OY 61 ttggccggccagatattctggcgggcaatgcctgttcgagcgtcatcttcaaccctcaagcc 120
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 313 ttggccggccagatattctggcggcgcacgctgttcgagcgtcatcttcaaccctcaagcc 372
OY 121 ccggggttgggtgttgggagcagcaag-cccttgcggaacccggcccggaatctagt 179
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

Db	273	CCCCGGCTTGTTGGAGATCGGCGTGCOCOCOCGGGGGGCGGCGNSCTCCCAATATAGT	4322
Qy	180	gcgagctcgcgtcagcttccatctcgtagtagtaaaacctcgcaactcgtacgcgcgcg	229
Db	433	GGCGGTCTCGCTGAGTCTTCTCTGCTGAGTACGACACTCGC---ACTGGAAACAGCG	489
Qy	240	cgagccagcgcttaaaccccccaactctc-aaagtctacctcgatcaggtagaataacc	238
Db	490	TGGCCACGCCCTTAAACCCCCCACTCTGAAAGTTGACCTCGGATCAGGTAGGAATACC	549
Qy	299	cgctgaactaa	310
Db	550	CGCTCAACTTAA	561

```

1 RESULT      6
2 US-08-652-127C-5
3 ; Sequence 5, Application US/08652127C
4 ; Patent No. 5792611
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: Richard C. Hamelin
8 ; TITLE OF INVENTION: DETECTION OF PLANT
9 ; TITLE OF INVENTION: PATHOGEN FUNGI
10 ; NUMBER OF SEQUENCES: 10
11 ;
12 ; CORRESPONDENCE ADDRESSES:
13 ; ADDRESSEE: George A. Seaby
14 ; ADDRESSEE: Seaby & Maclean
15 ; STREET: 880 Wellington Street, Suite 708
16 ; CITY: Ottawa
17 ; COUNTRY: Canada
18 ;
19 ; ZIP: K1R 6K7
20 ;
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: 3.5 inch diskette
23 ; COMPUTER: IBM PC Compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: ASCII
26 ;
27 ; CURRENT APPLICATION DATA:
28 ; APPLICATION NUMBER: US/08/652,127C
29 ; FILING DATE: May 23, 1996
30 ; CLASSIFICATION: 435
31 ;
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: George A. Seaby
34 ; REGISTRATION NUMBER: 24,034
35 ; REFERENCE/DOCKET NUMBER: 1898
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: (613) 232-5815
38 ; TELEFAX: (613) 232-5831
39 ; INFORMATION FOR SEQ ID NO: 5:
40 ; SEQUENCE CHARACTERISTICS:
41 ; LENGTH: 594
42 ; TYPE: nucleic acid
43 ; STRANDEDNESS: double
44 ; TOPOLOGY: Linear
45 ;
46 ; US-08-652-127C-5

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	Query Match	Similarity	63.88	Score 197.8	DB 1	Length 594
	Best Local	Similarity	85.08	Pred. No. 2.9e-55		
	Matches 271	Conservative	0	Mismatches 37	Indels 11	Gaps
Qy	1	aaagcgataagtaatgtaatgcaaatatcagatgatacatcgaaatcttgaagcaca	60			
Db	258	AAATGCGATAGTAAATGGAATTCGAGATTCAATGAAATCATCGAATCTTTGAAGCGACA	317			
Qy	61	tttgcgcccgcagatattcttgcgcgagcatgcctgttgcagcgtaattcaacctcaagcc	120			
Db	318	TTTGCGCCGCGCAGATTCGTGCGCGGATGCTGTTCAGAGCGTCATTTCAACCCCTCAAGCA	377			
Qy	121	cc-----cgggtttgtgttgggagatcgagcaag-----cccttgcgagcaagccggccggaa	172			
Db	378	CTTTCGGGAGCTTGCTGTGGGGGATCCGGCAGGCGGTCTCTCCGGGTCCGCGCGTCCCCCA	437			
Qy	173	atcagatgacgagtcgcctgcagatccatcttgacgtatglaaacaacctgcgaactgta	232			

D_b 438 ATCTAGTGGCGGTTCCGTGACCTTCCTGCCTAATAATACA - CCTGGCTCTGGAGT 495
 |||||
O_y 233 CGCGGCGGCGCAAGCGCTTAACCCCCAACCTCtgaat-gltgacctcgagatcaggtag 291
 |||||
D_b 496 CTCGGTGCGGCCACGCGCTAAACCCCACCACACTTTTTCTGCTGTACCTGAATCAGGTAG 555
 |||||
O_y 292 gaataccgcctgtaacttaa 310
 |||||
D_b 556 GACTACCGCTGAAGATTAA 574
 |||||

```

1 RESULT 7
2 US-08-887-480-96
3 ; Sequence 96, Application US/08887480
4 ; Patent No. 5814453
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: Beck, James J
8 ; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
9 ; TITLE OF INVENTION: polymerase Chain Reaction
10 ; NUMBER OF SEQUENCES: 96
11 ;
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: No. 5814453artis Corporation
14 ; STREET: 520 White Plains Road
15 ; CITY: Tarrytown
16 ; STATE: NY
17 ; COUNTRY: USA
18 ; ZIP: 10591
19 ;
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: floppy disk
22 ; COMPUTER: IBM PC compatible
23 ; OPERATING SYSTEM: PC-DOS/MS-DOS
24 ; SOFTWARE: Patentin Release #1.0, Version #1.25
25 ; CURRENT APPLICATION DATA:
26 ; APPLICATION NUMBER: US/08/887,480
27 ; FILING DATE:
28 ; CLASSIFICATION: 435
29 ; PRIOR APPLICATION DATA:
30 ; APPLICATION NUMBER: US 08/722,187
31 ; FILING DATE: 15-OCT-1996
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: Meigs, J. Timothy
34 ; REGISTRATION NUMBER: 38,241
35 ; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: 919-541-8587
38 ; TELEFAX: 919-541-8689
39 ; INFORMATION FOR SEQ ID NO: 96:
40 ;
41 ; SEQUENCE CHARACTERISTICS:
42 ; LENGTH: 546 base pairs
43 ; TYPE: nucleic acid
44 ; STRANDEDNESS: single
45 ; TOPOLOGY: linear
46 ; MOLECULE TYPE: DNA (genomic)
47 ; ORIGINAL SOURCE:
48 ; STRAIN: Fusarium poae
49 ; INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
50 ; INDIVIDUAL ISOLATE: sequence)
51 ; IMMEDIATE SOURCE:
52 ; CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
53 ; CLONE: pCRFpoaeT756(3-1)
54 ; FEATURE:
55 ; NAME/KEY: misc_feature
56 ; LOCATION: 1..30
57 ; OTHER INFORMATION: /note= "3' end of small subunit
58 ; OTHER INFORMATION: rRNA gene"
59 ; FEATURE:
60 ; NAME/KEY: misc_feature
61 ; LOCATION: 31..180
62 ; OTHER INFORMATION: /note= "ITS 1"
63 ; FEATURE:
64 ; NAME/KEY: misc_feature
65 ; LOCATION: 181..337
66 ;

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:
: OTHER INFORMATION: /note= "5.8S rRNA gene"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 338..489
:   OTHER INFORMATION: /note= "ITS 2"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 490..546
:   OTHER INFORMATION: /note= "5' end of large subunit"
:
: OTHER INFORMATION: rRNA gene"
:
US-08-887-480-96

Query Match      60.5%; Score 187.6; DB 1; Length 546;
Best Local Similarity 84.5%; Pred. No. 5.8e-52;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

OY 1 aatgagataaataatgtaattgcaaaaatcagatgacatcgaattcttgaagcaca 60
    |||||||
DB 231 AATGCGATAGTAAGTGAATGCGAATTCAGATTCAGATTCGAAATCTTTGAACGCACA 290

OY 61 ttgcgcccgcagatctctgcgagggcagtcgtctgcagcgtcatctcaaccctcaagcc 120
    |||||||
DB 291 TTGCGCGCCCGCAGTATTCGGCGGCGATGCTTTCGAGCGTCATTTCAACCCCTCAAGCC 350

OY 121 cccgggttggtgtgtgggagtcgcaagcccttcgcaagccgcgcgcgaatctagt 180
    |||||||
DB 351 C--ACCTTGCTGTGGG-----ATCTGTGCAACACAGTCCCAATTTGATTG 398

OY 181 gcgatctgcagatctcattcgtgtagtaaaacctcgcaacgtgtagcgggcgc 240
    |||||||
DB 399 GCGGTACG-TCGAGCTTCCATAGCGTATTTACACATGCTTACGTGATGCTGCG 457

OY 241 ggcgaagccgttaaaccccccaacttcgaatgtgacctcgatcgaatgaagaaatccgc 300
    |||||||
DB 458 GGCACGCGCGTTAA-CCCCAATTCTGAATGTGACCTCGGATCAGGTAGAGATACCGC 516

OY 301 ctgaactaa 310
    |||||||
DB 517 CTGAACCTTAA 526

RESULT 8
US-08-905-314A-22
: Sequence 22, Application US/08905314A
: Patent No. 5827695
: GENERAL INFORMATION:
:   APPLICANT: Beck, James J.
:   TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
:   TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
:   NUMBER OF SEQUENCES: 24
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: No. 5827695artis Corporation Patent Department
:     STREET: 3054 Cornwallis Road
:     CITY: Research Triangle Park
:     STATE: NC
:   COUNTRY: USA
:   ZIP: 20779-2257
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: PC-DOS/MS-DOS
:     SOFTWARE: Patentin Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/905.314A
:     FILING DATE:
:     CLASSIFICATION: 435
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Meigs, J. Timothy
:     REGISTRATION NUMBER: 38,241
:     REFERENCE/DOCKET NUMBER: CGC 1944
:     TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (919) 541-8587
```

```

:
: TELEFAX: (919) 541-8689
:
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 546 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
:   ORGANISM: Fusarium poae
:   INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
:   INDIVIDUAL ISOLATE: sequence)
: IMMEDIATE SOURCE:
:   CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
:   CLONE: pCRFpoaeT756(3-1)
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 1..30
:   OTHER INFORMATION: /note= "3' end of small subunit"
:   OTHER INFORMATION: rRNA gene"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 31..180
:   OTHER INFORMATION: /note= "ITS 1"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 181..337
:   OTHER INFORMATION: /note= "5.8S rRNA gene"
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 338..489
:   OTHER INFORMATION: /note= "ITS 2"
:
: NAME/KEY: misc_feature
: LOCATION: 490..546
: OTHER INFORMATION: /note= "5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
:
US-08-905-314A-22

Query Match      60.5%; Score 187.6; DB 1; Length 546;
Best Local Similarity 84.5%; Pred. No. 5.8e-52;
Matches 262; Conservative 0; Mismatches 34; Indels 14; Gaps 4;

OY 1 aatgagataaataatgtaattgcaaaaatcagatgacatcgaattcttgaagcaca 60
    |||||||
DB 231 AATGCGATAGTAAGTGAATGCGAATTCAGATTCAGATTCGAAATCTTTGAACGCACA 290

OY 61 ttgcgcccgcagatctctgcgagggcagtcgtctgcagcgtcatctcaaccctcaagcc 120
    |||||||
DB 291 TTGCGCGCCCGCAGTATTCGGCGGCGATGCTTTCGAGCGTCATTTCAACCCCTCAAGCC 350

OY 121 cccgggttggtgtgtgggagtcgcaagcccttcgcaagccgcgcgcgaatctagt 180
    |||||||
DB 351 C--AGCTTGCTGTGGG-----ATCTGTGCAACACAGTCCCAATTTGATTG 398

OY 181 gcgatctgcagatctcattcgtgtagtaaaacctcgcaacgtgtagcgggcgc 240
    |||||||
DB 399 GCGGTACG-TCGAGCTTCCATAGCGTATTTACACATGCTTACGTGATGCTGCG 457

OY 241 ggcgaagccgttaaaccccccaacttcgaatgtgacctcgatcgaatgaagaaatccgc 300
    |||||||
DB 458 GGCACGCGCGTTAA-CCCCAATTCTGAATGTGACCTCGGATCAGGTAGAGATACCGC 516

OY 301 ctgaactaa 310
    |||||||
DB 517 CTGAACCTTAA 526

RESULT 9
US-08-887-480-82
: Sequence 82, Application US/08887480
: Patent No. 5814453
```



```

: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04712
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/233,608
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Walsh, Andrea C.
: REGISTRATION NUMBER: 34,988
: REFERENCE/DOCKET NUMBER: CGC 1739
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8666
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 82:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 504 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1..504
: OTHER INFORMATION: /note="DNA sequence for the
: OTHER INFORMATION: Internal transcribed spacer region of Fusarium culmorum
: OTHER INFORMATION: (fcuim.con)"
PCT-US95-04712-82

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Query Match          60.2%; Score 186.6; DB 5; Length 504;
Best Local Similarity 82.6%; Pred. No. 1.2e-51;
Matches 252; Conservative 1; Mismatches 40; Indels 12; Gaps 3;

QY 1 aatgagataagtaatgtaattgcaaaattcagtgatcatcgaatccttgaagcaca 60
DB 212 AATGCGATGAATGAATGCAATTCAGATGCAATTCAGATTCATTGTTTAAACGCACA 271
QY 61 ttgcgcccgaatattctgcgcgcatgctctgagcgatcatttcaaccctcaagcc 120
DB 272 TTGCGCCCGCATATTCTGCGCGCATGCTCTTGTGACGCTATTTCACCTCAAGCC 331
QY 121 ccgaggcttggtgtgaggatcggaagcccttgcggaagccgcccgaatctagt 180
DB 332 C--ACCTTCGTGTGG-----AGCTGCAGTCTCTGTCACCTCCCAATATCATTTG 380
QY 181 gcggtctgctgagcttcattgtagtaaaaccttcgcaactgtgtacggggc 240
DB 381 GCGGTACGTCGATGCTTCATAGCTGATTAATTAATATGTTACTGTGATGCTGCC 440
QY 241 ggcgaagcgtttaaaccccaacttcgaatgtgaacctcgagtcagtaagataccg 300
DB 441 GCGYACGCGGTAA--CCCACTTCTGAATGTGACCTCGGATCAGTAGAATAACCGC 499
QY 301 ctgaa 305
DB 500 CTGAA 504

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RESULT 13
US-08-986-727-4
: Sequence 4, Application US/08986727
: Patent No. 6080543
: GENERAL INFORMATION:
: APPLICANT: ENGEL, Stacia R.
: APPLICANT: DESCENZO, Richard A.
: APPLICANT: IRELAN, Nancy A.
: TITLE OF INVENTION: DETECTION OF FUNGAL PATHOGENS

```

```

: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/986,727
: FILING DATE: 08-DEC-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ekstrom, Richard C.
: REGISTRATION NUMBER: 37,027
: REFERENCE/DOCKET NUMBER: 009773-012
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-6620
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 611 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-986-727-4

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Query Match          59.7%; Score 185; DB 3; Length 611;
Best Local Similarity 83.1%; Pred. No. 4.3e-51;
Matches 260; Conservative 0; Mismatches 45; Indels 8; Gaps 4;

QY 1 aatgagataagtaatgtaattgcaaaattcagtgatcatcgaatccttgaagcaca 60
DB 283 AATGCGATGAATGAATGCAATTCAGATGCAATTCAGATTCATTGTTTAAACGCACA 342
QY 61 ttgcgcccgaatattctgcgcgcatgctctgagcgatcatttcaaccctcaagcc 120
DB 343 TTGCGCCCTCTGATTCGAGGAGCATGCTGTTCCAGCTCATTTCAACCTCAAG-- 400
QY 121 ccgaggcttggtgtgaggatcggaagcccttgcggaagccgcccgaatctagt 180
DB 401 -CTGGCTTGGTGAATGGGCACTGCTCCCGCCCGGAGACAGGCCCTGAATCAGTG 459
QY 181 gcggtctgctgagcttcattgtagtaaaaccttcgcaactgtgtacggggc 238
DB 460 GCGACTCTGC--CAGGACCCCGAGCGCAGTAGTTAAACCTCTCGGAGGCCCTGCG 517
QY 239 ggcgcaagcgtttaaaccccaacttcgaatg-ttgaacctgagtcagtaagaaac 297
DB 518 GGTGCGCTGCGGTAAACCCCACTTCTGAAGTTTGACTCGATCAGTAGAATATAC 577
QY 298 ccgctgaactaa 310
DB 578 CCGCTGAACCTTAA 590

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RESULT 14
US-08-887-480-84
: Sequence 84, Application US/08887480
: Patent No. 5814453
: GENERAL INFORMATION:
: APPLICANT: Beck, James J
: TITLE OF INVENTION: Detection of Fungal Pathogens Using the
: NUMBER OF SEQUENCES: 96
: CORRESPONDENCE ADDRESS:

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; LOCATION: 179..335
; OTHER INFORMATION: /note= "5.8S rRNA gene"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 336..488
; OTHER INFORMATION: /note= "ITS 2"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 489..545
; OTHER INFORMATION: /note= "5' end of large subunit"
; OTHER INFORMATION: rRNA gene"
; US-08-905-314A-21
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Query Match

59.1%; Score 183.2; DB 1; Length 545;

Best Local Similarity 83.5%; Pred. No. 1.6e-50;

Matches 259; Conservative 0; Mismatches 38; Indels 13; Gaps 4;

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QY 1 aaatgagataagtaatgtaattgcgaataatcagtaatcgaatccttgaagcaca 60
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Db 229 AAATGCCATAGTAATGTGTAATTGCAGAAATTCAGTAATCATCGAATCTTTGAACGCACA 288
   |||

QY 61 tgcgcccccaagtatctgcgagcatgctgttcgagcgatcattcaaccctcaagcc 120
   |||
Db 289 TTGCGCCCGCCAGATATTCTGCGGCATGCTGTTCGAGCGTATTCAACCTCAAGCC 348
   |||

QY 121 cccgggttgggtctggggaatcgcaagcccttcgcaagccgccccgaatctagtg 180
   |||
Db 349 C---AGCTTGTTGTGGG-----AGCTGCAGTCTGCTGCACATCCCAATACATGTG 397
   |||

QY 181 gcggttcgctgcagtttcgatgctgagtaagtaaaacctcgcaactgtaagcgcg 240
   |||
Db 398 GCGGTACG-TCGAGCTTCATAGCGTATTTACACATCGTTACTGTATATCGTGC 456
   |||

QY 241 gccaagccgltlaaaccaccaacttcgaatgtlgaacctgagatcagtaggaataccg 300
   |||
Db 457 GGCACGCGCCTTAA-CCCAACTTCTGAATGTTGACCTCGGATCAGTAGGAATACCCG 515
   |||

QY 301 ctgaacttaa 310
   |||
Db 516 CTGAACCTTA 525
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Search completed: August 21, 2002, 22:12:26
Job time: 5699 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:32 ; Search time 8184.59 Seconds

(without alignments)
47.581 Million cell updates/sec

Title: US-10-046-955-50

Sequence: 1 cgtcaatcgcgtccctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1	18	100.0	18	US-09-423-233-50	Sequence 50, Appl
2	18	100.0	382	US-09-241-427-3	Sequence 3, Appl
3	16.4	91.1	620	US-09-580-797-11	Sequence 11, Appl
4	15.4	85.6	25	US-09-954-427-166475	Sequence 166475,
5	15.4	85.6	25	US-60-233-166-166475	Sequence 166475,
6	15.4	85.6	6936	US-60-161-932-210	Sequence 210, App
7	15.4	85.6	6938	US-09-528-237A-186	Sequence 186, App
8	15.4	85.6	26475	US-60-161-932-109	Sequence 109, App
9	15.4	85.6	26475	US-09-528-237A-1558	Sequence 1558, Ap
10	15.4	85.6	36240	US-09-620-392-61180	Sequence 58840, A
11	15.4	85.6	41444	US-09-702-134-26530	Sequence 61180, A
12	15.4	85.6	41444	US-09-815-264-65941	Sequence 26530, A
13	15.4	85.6	41444	US-09-815-264-65941	Sequence 65941, A
14	15.4	85.6	128	PCT-US02-03987-996	Sequence 996, App
15	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
16	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
17	15.4	85.6	128	PCT-US02-03987-996	Sequence 996, App
18	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
19	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
20	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
21	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
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74	15.4	85.6	128	US-09-815-242-996	Sequence 996, App
75	15.4	85.6	128	US-09-815-242-996	Sequence 996, App

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32 14.8 82.2 432 27 US-09-684-016-148514 Sequence 148514,
33 14.8 82.2 438 18 US-09-440-687-17246 Sequence 17246, A
34 14.8 82.2 438 25 US-09-654-617-69363 Sequence 69363, A
35 14.8 82.2 438 27 US-09-684-016-69363 Sequence 69363, A
36 14.8 82.2 438 53 US-60-144-084-13320 Sequence 1320, Ap
37 14.8 82.2 460 16 US-09-270-849B-32774 Sequence 32774, A
38 14.8 82.2 463 22 US-09-572-409-35481 Sequence 35481, A
39 14.8 82.2 468 16 US-09-270-849B-53297 Sequence 53297, A
40 14.8 82.2 481 17 US-09-304-517A-228553 Sequence 228553,
41 14.8 82.2 481 17 US-09-371-146A-228553 Sequence 228553,
42 14.8 82.2 481 36 US-09-985-678-228553 Sequence 228553,
43 14.8 82.2 481 51 US-60-125-817-7043 Sequence 7043, Ap
44 14.8 82.2 482 18 US-09-404-520-17444 Sequence 17444, A
45 14.8 82.2 650 1 PCT-US00-32639-103 Sequence 103, App
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ALIGNMENTS

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RESULT 1
US-09-423-233-50
; Sequence 50, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-423-233-50
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Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 cgttaattcgcttcctc 18
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Db 1 cgttaattcgcttcctc 18
```

```
RESULT 2
US-09-241-427-3
; Sequence 3, Application US/09241427
; GENERAL INFORMATION:
; APPLICANT: Yechezkel Kashi et al.
; TITLE OF INVENTION: NUCLEIC ACID-BASED ASSAY AND KIT FOR THE
; TITLE OF INVENTION: DETECTION OF ALTERNARIA CONTAMINATION IN
; TITLE OF INVENTION: FOOD PRODUCTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2.
; SOFTWARE: Word for Windows version 3.11
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/241,427
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; TELEPHONE: 74/57
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-241-427-3
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Query Match 100.0%; Score 18; DB 16; Length 382;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 cgttaattcgcttcctc 18
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Db 287 cgttaattcgcttcctc 304
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RESULT 3
US-09-580-797-11
; Sequence 11, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hirths, Steven H.
; APPLICANT: Henry, Travis
; TITLE OF INVENTION: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Fusarium oxysporum
US-09-580-797-11
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Query Match 91.1%; Score 16.4; DB 22; Length 620;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 cgttaattcgcttcctc 18
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Db 478 cgttaattcgcttcctc 495
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RESULT 4
US-09-954-427-166475
; Sequence 166475, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittman
; APPLICANT: Alfmetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925863
US-09-954-427-166475
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Best Local Similarity 94.1%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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        ||||||||| |||||||
Db      9 gtaaatcgggtctcc 25
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RESULT      5
US-60-233-166-166475
; Sequence 166475, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA925863
US-60-233-166-166475
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Best Local Similarity 94.1%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
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        ||||||||| |||||||
Db      9 gtaaatcgggtctcc 25
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RESULT      6
US-60-161-932-210/c
; Sequence 210, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161,932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 6936
; TYPE: DNA
; ORGANISM: Drosophila
; US-60-161-932-210
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```
Query Match      85.6%; Score 15.4; DB 55; Length 6936;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 cgttaatcgcgtctc 17
        ||| ||||||||| |||
Db      5984 CGTTCATTCGCTTCCT 5968
```

```
RESULT      7
US-09-528-237A-186
; Sequence 186, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 6938
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-186
```

```
Query Match      85.6%; Score 15.4; DB 19; Length 6938;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 cgttaatcgcgtctc 17
        ||| ||||||||| |||
Db      954 cgttaatcgcgtctc 970
```

```
RESULT      8
US-60-161-932-109/c
; Sequence 109, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161,932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 26474
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-109
```

```
Query Match      85.6%; Score 15.4; DB 55; Length 26474;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 cgttaatcgcgtctc 17
        ||||||||| |||
Db      1502 CGTTAATTCGCTTCCT 1486
```

```
RESULT      9
US-09-528-237A-1558/c
; Sequence 1558, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
```

```
;; CURRENT APPLICATION NUMBER: US/09/528.237A
;; CURRENT FILING DATE: 2000-03-17
;; NUMBER OF SEQ ID NOS: 2926
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1558
;; LENGTH: 26475
;; TYPE: DNA
;; ORGANISM: Drosophila
US-09-528-237A-1558
```

```
Query Match      85.6%; Score 15.4; DB 19; Length 26475;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 gtaattcgcgttcct 17
          ||||||| |||||
Db      1503 CGTTAATTCGCTTTCCT 1487
```

```
RESULT 10
US-09-620-392-58840/C
; Sequence 58840, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovallik, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 58840
; LENGTH: 36240
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-58840
```

```
Query Match      85.6%; Score 15.4; DB 24; Length 36240;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          ||||||| |||||
Db      14875 GTTAATTCACGCTTCCTC 14859
```

```
RESULT 11
US-09-620-392-61180
; Sequence 61180, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovallik, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 61180
; LENGTH: 41444
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-61180
```

```
Query Match      85.6%; Score 15.4; DB 24; Length 41444;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          ||||||| |||||
Db      20643 gtaattcgcgttcctc 20659
```

```
RESULT 12
US-09-702-134-26530
; Sequence 26530, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovallik, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 26530
; LENGTH: 41444
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-26530
```

```
Query Match      85.6%; Score 15.4; DB 28; Length 41444;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          ||||||| |||||
Db      20643 gtaattcgcgttcctc 20659
```

```
RESULT 13
US-09-815-264-65941
; Sequence 65941, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshl, Jeffrey M.
; APPLICANT: Kovallik, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 65941
; LENGTH: 41444
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-65941
```

```
Query Match      85.6%; Score 15.4; DB 31; Length 41444;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttcctc 18
          ||||||| |||||
Db      20643 gtaattcgcgttcctc 20659
```



```
RESULT 14
PCT-US02-03987-996/c
; Sequence 996, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for identifying the target of a compound which inhibits c
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
PCT-US02-03987-996
```

```
Query Match      83.3%; Score 15; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 gtaattcggttc 16
Db 118 GTTAATTCGCGTTCC 104
```

```
RESULT 15
US-09-815-242-996/c
; Sequence 996, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 996
; LENGTH: 128
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-996
```

```
Query Match      83.3%; Score 15; DB 31; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 gtaattcggttc 16
Db 118 GTTAATTCGCGTTCC 104
```

```
Search completed: August 22, 2002, 00:39:40
Job time: 13065 sec
```


GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: August 22, 2002, 00:50:53 ; Search time 663.62 Seconds
(without alignments)
72.981 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcgtctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 172111 seqs, 1345317543 residues

3442222

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents, NA, New: *
1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq: *
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq: *
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	7	US-10-046-955-50
2	14.4	80.0	25	5	US-09-956-604-95112
3	14.4	80.0	25	5	US-09-956-604-95113
4	14.4	80.0	26	5	US-09-975-254-9537
5	14.4	80.0	270	5	US-09-975-254-21902
6	14.4	80.0	651	7	US-10-027-632-266929
7	14.4	80.0	914	8	US-06-360-039-35000
8	14.4	77.8	2569	8	US-06-360-039-35000
9	13.8	76.7	251	5	US-09-975-254-30190
10	13.8	76.7	255	5	US-09-975-254-17320
11	13.8	76.7	255	5	US-09-975-254-17324
12	13.8	76.7	263	5	US-09-975-254-7020
13	13.8	76.7	366	6	US-10-098-754-13158
14	13.8	76.7	563	7	US-10-027-632-61031
15	13.8	76.7	563	7	US-10-027-632-309725
16	13.8	76.7	663	7	US-10-027-632-230673
17	13.8	76.7	774	8	US-06-360-039-29878
18	13.8	76.7	905	6	US-10-098-754-18470
19	13.8	76.7	1163	8	US-06-360-039-30593
20	13.8	76.7	1248	5	US-09-540-2098-168
21	13.8	76.7	3854	6	US-10-205-219-186
22	13.8	76.7	6642	5	US-09-545-199F-80
23	13.8	76.7	9423	7	US-10-101-840-6
24	13.8	76.7	9704	7	US-10-109-860-3
25	13.8	76.7	12666	7	US-10-158-844-137

ALIGNMENTS

26	13.8	76.7	13046	7	US-10-125-540-595	Sequence 595, App
27	13.8	76.7	24607	7	US-10-027-632-76188	Sequence 76188, A
28	13.8	76.7	49650	6	US-10-053-853A-410	Sequence 410, App
29	13.8	76.7	49795	6	US-10-114-170-60	Sequence 60, App
30	13.8	76.7	185548	1	PCT-US02-19457-62	Sequence 62, App
31	13.8	76.7	185548	7	US-10-175-523-62	Sequence 17011, A
32	13.4	74.4	349	5	US-09-721-544-17011	Sequence 14313, A
33	13.4	74.4	435	5	US-09-785-276A-14313	Sequence 35427, A
34	13.4	74.4	455	5	US-09-785-276A-35427	Sequence 44259, A
35	13.4	74.4	455	5	US-09-785-276A-44259	Sequence 5144, App
36	13.4	74.4	457	5	US-09-785-276A-5144	Sequence 22342, A
37	13.4	74.4	466	5	US-09-918-995-22342	Sequence 54492, A
38	13.4	74.4	608	5	US-09-785-276A-54492	Sequence 1236, App
39	13.4	74.4	665	8	US-06-377-240-1236	Sequence 29125, A
40	13.4	74.4	686	5	US-09-785-276A-29125	Sequence 34823, A
41	13.4	74.4	686	5	US-09-785-276A-34823	Sequence 8724, App
42	13.4	74.4	902	8	US-10-198-846-8724	Sequence 5152, App
43	13.4	74.4	1089	5	US-09-540-2098-5152	Sequence 261, App
44	13.4	74.4	1196	7	US-10-137-337-261	
45	13.4	74.4				

RESULT 1
US-10-046-955-50

Sequence 50, Application US/10046955

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as Represented by the

APPLICANT: Secretary of the Department of Health and Human Services, Centers for

APPLICANT: Control and Prevention

APPLICANT: Morrison, Christine J.

APPLICANT: Reiss, Errol

APPLICANT: Aldorevich, Lilliana

APPLICANT: Choi, Jong Soo

TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and

TITLE OF INVENTION: Other Filamentous Fungi

FILE REFERENCE: 6395-62064

CURRENT APPLICATION NUMBER: US/10/046,955

CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: US 09/423,233

PRIOR FILING DATE: 2000-06-27

PRIOR APPLICATION NUMBER: PCT/US98/08926

PRIOR FILING DATE: 1998-05-01

PRIOR APPLICATION NUMBER: US 60/045,400

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 50

TYPE: DNA

ORGANISM: Fusarium oxysporum

US-10-046-955-50

Query Match 100.0% ; Score 18 ; DB 7 ; Length 18 ;

Best Local Similarity 100.0% ; Pred. No. 1.7 ;

Matches 18 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

OY 1 cgttaatcgcgtctc 18

Db 1 cgttaatcgcgtctc 18

RESULT 2
US-09-956-604-95112/C

Sequence 95112, Application US/09956604

GENERAL INFORMATION:

APPLICANT: Miltmann, Michael

TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli

FILE REFERENCE: 3117.1

CURRENT APPLICATION NUMBER: US/09/956,604

```
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95112
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-95112
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ttaattcgcgcttcctc 18
    |||
Db 16 TTAAATCGCGTTCCTC 1
```

```
RESULT 3
US-09-956-604-95113/C
; Sequence 95113, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-95113
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ttaattcgcgcttcctc 18
    |||
Db 20 TTAAATCGCGTTCCTC 5
```

```
RESULT 4
US-09-975-254-9537
; Sequence 9537, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 9537
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700756034H1
US-09-975-254-9537
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 266;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ttaattcgcgcttcctc 18
    |||
Db 7 ttgattcgcgcttcctc 22
```

```
RESULT 5
US-09-975-254-21902
; Sequence 21902, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 21902
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700960259H1
US-09-975-254-21902
```

```
Query Match      80.0%; Score 14.4; DB 5; Length 270;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ttaattcgcgcttcctc 18
    |||
Db 43 ttgattcgcgcttcctc 58
```

```
RESULT 6
US-10-027-632-266929/C
; Sequence 266929, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266929
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-266929
```

Query Match 80.0%; Score 14.4; DB 7; Length 651;
Best Local Similarity 93.8%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gtaattcgcgtctt 17
||||| |||||||
DB 312 GTTAATGCCGCTTCT 297

RESULT 7

US-60-360-039-35000
; Sequence 35000, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360.039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35000
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Methanosarcina mazei
US-60-360-039-35000

Query Match 80.0%; Score 14.4; DB 8; Length 914;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gtaattcgcgtctt 17
||||| |||||||
DB 611 gtaattcgcgtctt 626

RESULT 8

US-60-360-039-36500
; Sequence 36500, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360.039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36500
; LENGTH: 2569
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-360-039-36500

Query Match 77.8%; Score 14; DB 8; Length 2569;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 aattcgcgtctt 18
||||| |||||||
DB 599 aattcgcgtctt 612

RESULT 9

US-09-975-254-30190
; Sequence 30190, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975.254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263.191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 30190
; LENGTH: 251
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700901009H1
US-09-975-254-30190

Query Match 76.7%; Score 13.8; DB 5; Length 251;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaattcgcgtctt 17
||||| |||||||
DB 52 cgttaattcgcgtctt 68

RESULT 10

US-09-975-254-17320
; Sequence 17320, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975.254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263.191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 17320
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700954206H1
US-09-975-254-17320

Query Match 76.7%; Score 13.8; DB 5; Length 255;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaattcgcgtctt 17
||||| |||||||
DB 170 cgttaattcgcgtctt 186

RESULT 11

US-09-975-254-17834
; Sequence 17834, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B

```
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 17834
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700954789H1
US-09-975-254-17834
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```
Query Match          76.7%; Score 13.8; DB 5; Length 255;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 cgttaatcgcgttct 17
         ||||||| |||||
Db       169 cgttaatcattcttct 185
```

```
RESULT 12
US-09-975-254-7020
; Sequence 7020, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 7020
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700752705H1
US-09-975-254-7020
```

```
Query Match          76.7%; Score 13.8; DB 5; Length 263;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 cgttaatcgcgttct 17
         ||||||| |||||
Db       174 cgttaatcattcttct 190
```

```
RESULT 13
US-10-098-754-13158
; Sequence 13158, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
; APPLICANT: Ramachandran, Rakesh
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: ATX-001CN
; CURRENT APPLICATION NUMBER: US/10/098,754
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 21107
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13158
```

```
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(366)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-13158
```

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Query Match          76.7%; Score 13.8; DB 6; Length 366;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttctc 18
         ||||||| |||||
Db       294 gtaattccttcttc 310
```

```
RESULT 14
US-10-027-632-61031/C
; Sequence 61031, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61031
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-61031
```

```
Query Match          76.7%; Score 13.8; DB 7; Length 563;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 gtaattcgcgttctc 18
         ||||| ||||||| ||
Db       162 gtttaagtcgcgttcttc 146
```

```
RESULT 15
US-10-027-632-309725/C
; Sequence 309725, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 309725
: LENGTH: 563
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-309725

Query Match 76.7%; Score 13.8; DB 7; Length 563;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 2 gtaatcgcgttcctc 18
||||| ||||| |||
Db 162 CTTAAGTCGCCTTCTTC 146

Search completed: August 22, 2002, 00:50:57
Job time: 11897 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:51 ; Search time 2238.68 Seconds

(Without alignments)
196.302 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaacacctgcactgagaga 21

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	21	100.0	319	8	AF117921	AF117921 Nectria h
2	21	100.0	471	8	AF161222	AF161222 Fusarium
3	21	100.0	471	8	AY043472	AY043472 Haematone
4	21	100.0	471	8	AY043473	AY043473 Haematone
5	21	100.0	471	8	AY043478	AY043478 Haematone
6	21	100.0	477	8	FSU38558	U38558 Fusarium so
7	21	100.0	478	8	AF132801	AF132801 Nectria h
8	21	100.0	478	8	AF150459	AF150459 Nectria h
9	21	100.0	478	8	AF150460	AF150460 Nectria h
10	21	100.0	478	8	AF150461	AF150461 Nectria h
11	21	100.0	478	8	AF150462	AF150462 Nectria h
12	21	100.0	478	8	AF150463	AF150463 Nectria h
13	21	100.0	478	8	AF150464	AF150464 Nectria h
14	21	100.0	478	8	AF150465	AF150465 Nectria h
15	21	100.0	479	8	AF150469	AF150469 Nectria h
16	21	100.0	479	8	AF150470	AF150470 Nectria h
17	21	100.0	479	8	AF150475	AF150475 Nectria h
18	21	100.0	480	8	AF150466	AF150466 Nectria h
19	21	100.0	480	8	AF150467	AF150467 Nectria h
20	21	100.0	480	8	AF150477	AF150477 Nectria h
21	21	100.0	480	8	AF150478	AF150478 Nectria h
22	21	100.0	480	8	AF150479	AF150479 Nectria h
23	21	100.0	480	8	AF150480	AF150480 Nectria h
24	21	100.0	480	8	AF440567	AF440567 Nectria h
25	21	100.0	483	8	FSU38557	U38557 Fusarium so
26	21	100.0	483	8	AY043477	AY043477 Haematone
27	21	100.0	505	8	AY043470	AY043470 Haematone
28	21	100.0	509	8	AF165874	AF165874 Nectria h
29	21	100.0	544	8	NEXTS	L36627 Neocosmospo
30	21	100.0	546	8	AF178413	AF178413 Neocosmos
31	21	100.0	547	8	AF178412	AF178412 Neocosmos
32	21	100.0	547	8	NECTISA	L36619 Nectria hae
33	21	100.0	548	8	AF178397	AF178397 Fusarium
34	21	100.0	548	8	AF178402	AF178402 Fusarium
35	21	100.0	549	8	AF178398	AF178398 Nectria 1
36	21	100.0	550	8	AF178394	AF178394 Nectria 1
37	21	100.0	550	8	AF178401	AF178401 Nectria h
38	21	100.0	550	8	AF178407	AF178407 Fusarium
39	21	100.0	550	8	AF178408	AF178408 Fusarium
40	21	100.0	550	8	AF178422	AF178422 Fusarium
41	21	100.0	569	8	AF129104	AF129104 Nectria h
42	20	95.2	471	8	AY043469	AY043469 Haematone
43	20	95.2	471	8	AY043476	AY043476 Haematone
44	20	95.2	475	8	AY043475	AY043475 Haematone
45	19.4	92.4	477	8	AY043474	AY043474 Haematone

ALIGNMENTS

RESULT 1
AF117921
LOCUS AF117921 319 bp DNA linear PLN 17-JUN-2000
DEFINITION Nectria haematococca 5.8S ribosomal RNA gene, partial sequence;
internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence.
ACCESSION AF117921 GI:8570107
VERSION AF117921.1 GI:8570107
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE
1 (bases 1 to 319)
Choi,J.S., Westerman,J.M. and Morrison,C.J.
Rapid differentiation of filamentous fungi using species-specific
DNA probes
Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
2 (bases 1 to 319)
Choi,J.S., Westerman,J.M. and Morrison,C.J.
Direct Submission
Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

FEATURES
source location/Qualifiers
1. .319
/organism="Nectria haematococca"
/db_xref="taxon:140110"
rRNA
160. .272
/product="5.8S ribosomal RNA"
misc_RNA
/note="ITS2"
/product="internal transcribed spacer 2"
273. .>319
/product="28S ribosomal RNA"
BASE COUNT 77 a 96 c 84 g 62 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 319;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgactggaga 21
|||||
Db 222 CTAACACTCGCACTGAGAG 242

RESULT 2
AF161222 471 bp DNA linear PLN 09-FEB-2000
LOCUS
DEFINITION Fusarium solani internal transcribed spacer 1, partial sequence;
5.8S ribosomal RNA gene, complete sequence; internal transcribed
spacer 2, and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF161222 GI:6941832
VERSION
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE
AUTHORS 1 (bases 1 to 471)
TITLE Grunden, E., Chen, W., and Crane, J. L.
JOURNAL Fungi Colonizing Microsclerotia of Verticillium dahliae
REFERENCE 2 (bases 1 to 471)
AUTHORS Grunden, E., Chen, W., and Crane, J. L.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1999) Center for Biodiversity, Illinois Natural
History Survey, IL Dept. Natural Resources, 607 E. Peabody Dr.,
Champaign, IL 61820, USA
FEATURES
source location/Qualifiers
1. .471
/organism="Nectria haematococca"
/db_xref="taxon:140110"
misc_RNA
/note="ITS1"
/product="internal transcribed spacer 1"
118. .276
/product="5.8S ribosomal RNA"
277. .450
/note="ITS2"
/product="internal transcribed spacer 2"
451. .>471
/product="28S ribosomal RNA"
BASE COUNT 121 a 133 c 117 g 100 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgactggaga 21
|||||
Db 390 CTAACACTCGCACTGAGAG 410

RESULT 3
AY043472/c 471 bp DNA linear PLN 05-SEP-2001
LOCUS
DEFINITION Haematonectria haematococca strain 35 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AY043472
VERSION AY043472.1 GI:15450333
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE
AUTHORS 1 (bases 1 to 471)
TITLE Miller, R.N.G. and Lopes, C.A.
JOURNAL rDNA sequence variability in Fusarium solani populations associated
with eumartii wilt and dry rot of potato in Brazil
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil
FEATURES
source location/Qualifiers
1. .471
/organism="Nectria haematococca"
/strain="35"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
/note="contains internal transcribed spacer 1, 5.8S
ribosomal RNA, and internal transcribed spacer 2"
BASE COUNT 94 a 121 c 136 g 118 t 2 others
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgactggaga 21
|||||
Db 59 CTAACACTCGCACTGAGAG 39

RESULT 4
AY043473/c 471 bp DNA linear PLN 05-SEP-2001
LOCUS
DEFINITION Haematonectria haematococca strain 39 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AY043473
VERSION AY043473.1 GI:15450334
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE
AUTHORS 1 (bases 1 to 471)
TITLE Miller, R.N.G. and Lopes, C.A.
JOURNAL rDNA sequence variability in Fusarium solani populations associated
with eumartii wilt and dry rot of potato in Brazil
REFERENCE 2 (bases 1 to 471)
AUTHORS Miller, R.N.G. and Lopes, C.A.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genomic Biotechnology, Universidade
Catolica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil
FEATURES
source location/Qualifiers
1. .471

/organism="Nectria haematococca"
/strain="39"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani!"
/note="contains internal transcribed spacer 1, 5.8S
ribosomal RNA, and internal transcribed spacer 2"
BASE COUNT 92 a 118 c 142 g 118 t 1 others
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
|||||
Db 60 CTACACCTCGCACTGAGAGA 40

RESULT 5
AY043478/c 471 bp DNA linear PLN 05-SEP-2001
LOCUS
DEFINITION Haematococca haematococca strain 83 internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AY043478
VERSION AY043478.1 GI:15450339
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Hypocreales; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Eukaryota; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 471)
AUTHORS Miller,R.N.G. and Lopes,C.A.
TITLE rDNA sequence variability in Fusarium solani populations associated
with eumartii wilt and dry rot of potato in Brazil
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 471)
TITLE Miller,R.N.G. and Lopes,C.A.
JOURNAL Direct Submission
SUBMITTED (03-JUL-2001) Genomic Biotechnology, Universidade
Catoilica de Brasilia, SGAN 916 Modulo B, Brasilia, DF 70790-160,
Brazil

FEATURES
source location/Qualifiers
1..471
/organism="Nectria haematococca"
/strain="83"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani!"
complement(1..471)
/note="contains internal transcribed spacer 1, 5.8S
ribosomal RNA, and internal transcribed spacer 2"
BASE COUNT 91 a 120 c 138 g 121 t 1 others
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 471;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
|||||
Db 59 CTACACCTCGCAACTGAGAGA 39

RESULT 6
FSU38558 477 bp DNA linear PLN 08-NOV-1995
LOCUS
DEFINITION Fusarium solani 5.8S ribosomal RNA gene, complete sequence and
internal transcribed spacers 1 and 2.
ACCESSION U38558
VERSION U38558.1 GI:1054930

KEYWORDS
SOURCE Fusarium solani.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 477)
AUTHORS Dugal,A.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1995) Arli Dugal, Forestry, Univ. of Toronto, 33
Willcocks St., Toronto, Ont. M5S 3B3, Canada

FEATURES
source location/Qualifiers
1..477
/organism="Nectria haematococca"
/db_xref="taxon:140110"
1..150
/note="internal transcribed spacer 1; ITS1"
151..306
/product="5.8S ribosomal RNA"
307..477
/note="internal transcribed spacer 2; ITS2"
BASE COUNT 122 a 143 c 114 g 96 t 2 others
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 477;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
|||||
Db 418 CTACACCTCGCACTGAGAGA 438

RESULT 7
AF132801 478 bp DNA linear PLN 20-JAN-2000
LOCUS
DEFINITION Nectria haematococca internal transcribed spacer 1, 5.8S ribosomal
RNA, and internal transcribed spacer 2, complete sequence.
ACCESSION AF132801
VERSION AF132801.1 GI:4809015
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
AUTHORS Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.
TITLE Molecular identification of Fungi Associated with Vascular
Discoloration of Soybean in the North Central United States
JOURNAL Plant Dis. 84 (1), 83-89 (2000)
AUTHORS 2 (bases 1 to 478)
TITLE Harrington,T.C., Steimel,J.P., Workneh,F. and Yang,X.B.
JOURNAL Direct Submission
SUBMITTED (03-MAR-1999) Plant Pathology, Iowa State University,
Room 351 Bessey Hall, Ames, IA 50011, USA

FEATURES
source location/Qualifiers
1..478
/organism="Nectria haematococca"
/isolate="P185"
/specific_host="Glycine max"
/db_xref="taxon:140110"
/tissue_type="mycelium"
/country="USA: Iowa, Lee County"
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/note="ITS1"
/product="internal transcribed spacer 1"
150..306
/product="5.8S ribosomal RNA"
307..478
/note="ITS2"
/product="internal transcribed spacer 2"
BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgaga 21
|||||
Db 419 CTAACACCTCGCACTGAGA 439

RESULT 8
AF150459 478 bp DNA linear PLN 05-JAN-2001
LOCUS
DEFINITION Nectria haematococca strain K-1 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150459
VERSION AF150459.1 GI:7650157
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
FEATURES
source
1. 478
/organism="Nectria haematococca"
/strain="K-1"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
1. 149
/product="internal transcribed spacer 1"
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rRNA /product="5.8S ribosomal RNA"
308..478
misc_RNA /product="internal transcribed spacer 2"
BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgaga 21
|||||
Db 419 CTAACACCTCGCACTGAGA 439

RESULT 9
AF150460 478 bp DNA linear PLN 05-JAN-2001
LOCUS
DEFINITION Nectria haematococca strain F1 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150460
VERSION AF150460.1 GI:7650158
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)

AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
FEATURES
source
1. 478
/organism="Nectria haematococca"
/strain="F1"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
1. 149
/product="internal transcribed spacer 1"
150..307
rRNA /product="5.8S ribosomal RNA"
308..478
misc_RNA /product="internal transcribed spacer 2"
BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgaga 21
|||||
Db 419 CTAACACCTCGCACTGAGA 439

RESULT 10
AF150461 478 bp DNA linear PLN 05-JAN-2001
LOCUS
DEFINITION Nectria haematococca strain F4 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF150461
VERSION AF150461.1 GI:7650159
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan
FEATURES
source
1. 478
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/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
1. 149
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150..307
rRNA /product="5.8S ribosomal RNA"
308..478
misc_RNA /product="internal transcribed spacer 2"
BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaacacctgcgaactggaga 21
|||||
Db 419 CTACACCTCGCACTGGAGA 439

RESULT 11

AF150462 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SW1 internal transcribed spacer 1, 5.8S
DEFINITION ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
AF150462
ACCESSION AF150462.1 GI:7650160
VERSION
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
JOURNAL based on the rDNA-ITS region
AUTHORS Mycol. Res. 104 (10), 1175-1183 (2000)
TITLE 2 (bases 1 to 478)
JOURNAL Suga,H., Hyakumachi,M. and Kageyama,K.
AUTHORS Direct Submission
TITLE Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
JOURNAL University, Gifu 501-1112, Japan
FEATURES
source
1. .478
/organism="Nectria haematococca"
/strain="SW1"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani"
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/product="internal transcribed spacer 1"
rRNA
150. .307
/product="5.8S ribosomal RNA"
misc_RNA
308. .478
/product="internal transcribed spacer 2"
BASE COUNT 123 a 138 c 115 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaacacctgcgaactggaga 21
|||||
Db 419 CTACACCTCGCACTGGAGA 439

RESULT 12

AF150463 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SUF471 internal transcribed spacer 1,
DEFINITION 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
AF150463
ACCESSION AF150463.1 GI:7650161
VERSION
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani

JOURNAL based on the rDNA-ITS region
AUTHORS Mycol. Res. 104 (10), 1175-1183 (2000)
TITLE 2 (bases 1 to 478)
JOURNAL Suga,H., Hyakumachi,M. and Kageyama,K.
AUTHORS Direct Submission
TITLE Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
JOURNAL University, Gifu 501-1112, Japan
FEATURES
source
1. .478
/organism="Nectria haematococca"
/strain="SUF471"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani f. sp. radicola"
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/product="internal transcribed spacer 1"
rRNA
150. .307
/product="5.8S ribosomal RNA"
misc_RNA
308. .478
/product="internal transcribed spacer 2"
BASE COUNT 123 a 139 c 115 g 101 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;

QY 1 ctaacacctgcgaactggaga 21
|||||
Db 419 CTACACCTCGCACTGGAGA 439

RESULT 13

AF150464 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SUF208 internal transcribed spacer 1,
DEFINITION 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
AF150464
ACCESSION AF150464.1 GI:7650162
VERSION
KEYWORDS
SOURCE Nectria haematococca.
ORGANISM Nectria haematococca.
REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
JOURNAL based on the rDNA-ITS region
AUTHORS Mycol. Res. 104 (10), 1175-1183 (2000)
TITLE 2 (bases 1 to 478)
JOURNAL Suga,H., Hyakumachi,M. and Kageyama,K.
AUTHORS Direct Submission
TITLE Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
JOURNAL University, Gifu 501-1112, Japan
FEATURES
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1. .478
/organism="Nectria haematococca"
/strain="SUF208"
/db_xref="taxon:140110"
/note="anamorph: Fusarium solani f. sp. radicola"
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1. .149
/product="internal transcribed spacer 1"
rRNA
150. .307
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misc_RNA
308. .478
/product="internal transcribed spacer 2"
BASE COUNT 123 a 139 c 115 g 101 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
|||||
Db 419 CTAACACCTCGCACTGGAGA 439

RESULT 14
AF150465 478 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain SUF532 internal transcribed spacer 1,
DEFINITION 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF150465
VERSION AF150465.1 GI:7650163
KEYWORDS
SOURCE Nectria haematococca
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 478)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)
REFERENCE 2 (bases 1 to 478)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan

FEATURES
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1. .478
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/strain="SUF532"
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/note="anamorph: Fusarium solani f. sp. radiclecola"
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rRNA
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/product="5.8S ribosomal RNA"
308. .478
misc_RNA
/product="internal transcribed spacer 2"
BASE COUNT 124 a 138 c 114 g 102 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
|||||
Db 419 CTAACACCTCGCACTGGAGA 439

RESULT 15
AF150469 479 bp DNA linear PLN 05-JAN-2001
LOCUS Nectria haematococca strain MAFF236572 internal transcribed spacer
DEFINITION 1.5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence.
ACCESSION AF150469
VERSION AF150469.1 GI:7650167
KEYWORDS
SOURCE Nectria haematococca
ORGANISM Nectria haematococca
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.

REFERENCE 1 (bases 1 to 479)
AUTHORS Suga,H., Hasegawa,T., Mitsui,H., Kageyama,K. and Hyakumachi,M.
TITLE Phylogenetic analysis of phytopathogenic fungus, Fusarium solani
based on the rDNA-ITS region
JOURNAL Mycol. Res. 104 (10), 1175-1183 (2000)

REFERENCE 2 (bases 1 to 479)
AUTHORS Suga,H., Hyakumachi,M. and Kageyama,K.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Molecular Genetics Research Center, Gifu
University, Gifu 501-1112, Japan

FEATURES
source
1. .479
/organism="Nectria haematococca"
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/note="anamorph: Fusarium solani f. sp. piperis"
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152. .309
/product="5.8S ribosomal RNA"
310. .479
misc_RNA
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BASE COUNT 120 a 148 c 114 g 97 t
ORIGIN

Query Match 100.0%; Score 21; DB 8; Length 479;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactggaga 21
|||||
Db 419 CTAACACCTCGCACTGGAGA 439

Search completed: August 21, 2002, 22:09:51
Job time: 14205 sec

|

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:22:47 ; Search time 594.49 Seconds

(without alignments)
60.649 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctacacctgcacactgagaga 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	20	AAV83698
2	21	100.0	319	20	AAV70850
3	19	90.5	502	21	AAV61893
4	19	90.5	561	19	AAV59009
5	17	81.0	510	21	AAV37182
6	17	81.0	2706	22	AAV45891
7	16.2	77.1	33769	22	ABA82622
8	15.8	75.2	1399	23	ABL09973
9	15.8	75.2	1815	23	ABL02977

10	15.8	75.2	3399	23	ABL09972	Drosophila melanog
11	15.8	75.2	3405	24	AAV59263	Long terminal repe
12	15.8	75.2	3947	23	ABL02976	Drosophila melanog
13	15.8	75.2	4344	23	ABL08778	Drosophila melanog
14	15.8	75.2	4763	23	ABL08780	Drosophila melanog
15	15.4	73.3	989	23	ABL18503	Drosophila melanog
16	15.4	73.3	1260	23	ABL11645	Drosophila melanog
17	15.4	73.3	1884	23	AAV5358	Drosophila melanog
18	15.4	73.3	2310	23	AAV52105	Staphylococcus aur
19	15.4	73.3	2700	23	AAV54538	Staphylococcus aur
20	15.4	73.3	2790	23	AAV51168	Staphylococcus aur
21	15.4	73.3	2853	23	ABL15238	Drosophila melanog
22	15.4	73.3	3061	23	ABL18502	Drosophila melanog
23	15.4	73.3	3433	23	ABL11644	Drosophila melanog
24	15.4	73.3	3713	23	ABL15001	Drosophila melanog
25	15.4	73.3	4676	23	ABL08318	Drosophila melanog
26	15.4	73.3	6325	23	ABL06620	Drosophila melanog
27	15.4	73.3	29555	18	AAV74517	Staphylococcus aur
28	15.4	73.3	41723	23	ABL23684	Drosophila melanog
29	15.2	72.4	352	20	AAV86546	Human single nucle
30	15.2	72.4	352	20	AAV86548	Human single nucle
31	15.2	72.4	352	20	AAV86549	Human single nucle
32	15.2	72.4	551	22	AAV70030	Human immune/haema
33	15.2	72.4	551	22	AAV70031	Human immune/haema
34	15.2	72.4	1173	21	AAV294583	Maize cyclin D ZMC
35	15.2	72.4	1235	22	AAV59374	Human polynucleoti
36	15.2	72.4	1370	21	AAV50337	Arabidopsis thalia
37	15.2	72.4	1609	21	AAV46043	Arabidopsis thalia
38	15.2	72.4	1611	21	AAV33022	Arabidopsis thalia
39	15.2	72.4	1796	22	AAV89924	Human bone marrow
40	15.2	72.4	1800	22	AAV80351	Nucleotide sequenc
41	15.2	72.4	1932	20	AAV19961	Corn cyclin delta-
42	15.2	72.4	2366	23	ABL15104	Drosophila melanog
43	15.2	72.4	2726	22	ABA88958	Escherichia coli p
44	15.2	72.4	3070	23	ABL06688	Escherichia coli p
45	15.2	72.4	13757	22	ABA88957	Escherichia coli p

ALIGNMENTS

RESULT 1	
AAV83698	AAV83698 standard; DNA: 21 BP.
ID	AAV83698 standard; DNA: 21 BP.
XX	
AC	AAV83698;
XX	
DT	26-FEB-1999 (first entry)
XX	
DE	Species-specific probe targeted to the internal transcribed spacer 2.
XX	
KW	Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
KW	A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW	Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW	M. circinellioideus f. circinelloides; Rhizopus oryzae; R. microsporus;
KW	R. circinellus; R. stolonifer; Rhizomucor pusillus; Aspidia corymbifera;
KW	Cunninghamella elegans; Pseudallesheria boydii; Scedosporium apiospermum;
KW	Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX	
OS	Synthetic.
OS	Fusarium solani.
XX	
FT	Key
FT	modified_base 1
FT	Location/Qualifiers
FT	/*tag= a
FT	/note= "labelled with digoxigenin"
PN	WO9850584-A2.
XX	
PD	12-NOV-1998.
XX	
PF	01-MAY-1998; 98WO-US08926.
XX	

```

PR 02-MAY-1997: 97US-0045400.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX
DR WPI; 1999-034737/03.
XX
PT New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
PS Example 1: Page 22: 45pp: English.
XX
CC Probes AAV83677-708 are derived from the internal transcribed spacer 2
CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
CC are species-specific, and can be used for identifying a species selected
CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A.
CC nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M.
CC plumbeus, M. indicus, M. circinelloides f. circinelloides, Rhizopus
CC pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallescheria
CC boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
XX
SQ Sequence 21 BP: 7 A; 7 C; 4 G; 3 T; 0 other:

Query Match      100.0%; Score 21: DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactgaga 21
   |||
Db 1 ctacacctgcgaactgaga 21

RESULT 2
AAV70850
ID AAV70850 standard; DNA: 319 BP.
XX
AC AAV70850;
XX
DT 26-FEB-1999 (first entry)
XX
DE Internal transcribed spacer 2 (ITS2) and adjacent regions.
XX
KW Internal transcribed spacer 2; ITS2; probe: Aspergillus flavus;
KW A. niger; A. terreus; A. nidulans; Fusarium solani; F. moniliforme;
KW Mucor rouxii; M. racemosus; M. plumbeus; M. indicus; A. fumigatus;
KW M. circinelloides f. circinelloides; Rhizopus oryzae; R. microsporus;
KW R. circinans; R. stolonifer; Rhizomucor pusillus; Absidia corymbifera;
KW Cunninghamella elegans; Pseudallescheria boydii; Scedosporium apiospermum;
KW Penicillium notatum; Sporothrix schenckii; filamentous fungus; ss.
XX
OS Fusarium solani.
XX
PN WO9850584-A2.
XX
PD 12-NOV-1998.
XX
PP 01-MAY-1998: 98WO-US08926.
XX
PR 02-MAY-1997: 97US-0045400.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Aldorevich L, Choi JS, Morrison CJ, Reiss E;
XX
DR WPI; 1999-034737/03.

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XX
PT New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia,
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
PS Claim 1: Page 12: 45pp: English.
XX
CC The present sequence represents an internal transcribed spacer 2 (ITS2)
CC and adjacent regions. Probes can be derived from the present sequence
CC which are species-specific. The specification also describes ITS2
CC sequence-derived probes for identifying a species selected from
CC Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A. nidulans,
CC Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M. plumbeus,
CC R. indicus, M. circinelloides f. circinelloides, Rhizopus oryzae,
CC M. microsporus, R. circinans, R. stolonifer, Rhizomucor pusillus,
CC Absidia corymbifera, Cunninghamella elegans, Pseudallescheria boydii
CC (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
XX
SQ Sequence 319 BP: 77 A; 96 C; 84 G; 62 T; 0 other:

Query Match      100.0%; Score 21: DB 20; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacacctgcgaactgaga 21
   |||
Db 222 ctacacctgcgaactgaga 242

RESULT 3
AAA61893
ID AAA61893 standard; DNA: 502 BP.
XX
AC AAA61893;
XX
DT 14-NOV-2000 (first entry)
XX
DE Fusarium sp. MF6381 rDNA internal transcribed spacer (ITS) region.
XX
KW Ribosomal DNA; rDNA ITS region; internal transcribed spacer; ATCC 74469;
KW HIV integrase inhibitor; steroid compound; human immunodeficiency virus;
KW acquired immunodeficiency syndrome; AIDS; ARC; AIDS-related complex;
KW symptomatic infection; asymptomatic infection; potential HIV exposure;
KW combination therapy; ds.
XX
OS Fusarium sp. MF6381.
XX
PN WO200036132-A1.
XX
PD 22-JUN-2000.
XX
PP 09-DEC-1999: 99WO-US29356.
XX
PR 14-DEC-1998: 98US-0112168.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Singh SB, Zink DL, Hazuda DJ, Felock PJ, Polishook JD;
XX
PI Dombrowski AW;
XX
DR WPI; 2000-431606/37.
XX
PT New steroid compounds are HIV integrase inhibitors used for treating
PT HIV infection and AIDS -
XX
PS Disclosure: Page 14: 113pp: English.
XX
CC The invention relates to novel steroid compounds derived from the

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CC African soil fungus *Fusarium* sp. MF6381 (ATCC 74469) which act as
CC inhibitors of HIV integrase. The invention encompasses cultures of
CC *Fusarium* sp. MF6381. The invention also relates to a composition
CC comprising a compound of the invention in combination with an AIDS
CC antiviral agent, an immunomodulator and an antiinfective agent. The
CC compounds of the invention may be used in the inhibition of HIV
CC integrase and in the prevention and treatment of HIV infection. A wide
CC range of state of HIV infection may be treated: AIDS (acquired
CC immunodeficiency syndrome); ARC (AIDS-related complex); both symptomatic
CC and asymptomatic HIV infection; and actual or potential exposure to HIV.
CC The compounds may be used to isolate HIV integrase mutants which are
CC potentially useful as screening tools for antiviral compounds. The
CC compounds may also be used to establish or determine the site at which
CC other antivirals bind to HIV integrase (e.g., by competitive inhibition).
CC The present sequence represents the ribosomal DNA (rDNA) internal
CC transcribed spacer (ITS) region of *Fusarium* sp. MF6381, which may be used
CC to characterise MF6381.

SO Sequence 502 BP; 127 A; 144 C; 118 G; 113 T; 0 other;

Query Match 90.5%; Score 19; DB 21; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacacctgcgaactgga 19
|||||
Db 410 ctacacctgcgaactgga 428

RESULT 4

AAV59009
ID AAV59009 standard; DNA: 561 BP.

XX AAV59009;

DT 06-JAN-1999 (first entry)

XX F. avenaceum internal transcribed spacer.

XX Internal transcribed spacer; ITS; Microdochium; *Fusarium*; wheat pathogen;
KM fungal pathogen identification; infection identification; ss.

XX *Fusarium* avenaceum.

XX Key Location/Qualifiers

FT misc_feature 31..181

FT misc_feature /note="ITS1"

FT misc_feature 339..504

FT misc_feature /tag="b"

FT misc_feature /note="ITS2"

XX US5827695-A.

XX 27-OCT-1998.

XX 01-AUG-1997; 97US-0905314.

XX 01-AUG-1997; 97US-0905314.

XX (NOVS) NOVARTIS FINANCE CORP.

XX Beck JJ;

XX WPI; 1998-593995/50.

XX Wheat pathogen internal transcribed spacer sequences - used as a
PT basis for primers for the species-specific polymerase chain reaction
PT detection of the pathogens
XX Claim 1; Column 29-30; 20pp; English.

CC This sequence represents an internal transcribed spacer (ITS) sequence of
CC the invention. The primer pairs, based on the ITS sequences, are used for
CC the PCR amplification detection of wheat *Microdochium* and *Fusarium* fungal
CC pathogens, especially *M. nivale*, *F. graminearum*, *F. culmorum*,
CC *F. avenaceum*, *F. poae*, *F. moniliforme* or *F. roseum*. The two different
CC strains of fungi show different symptoms during infection, which may or
CC may not be due to infection. Early identification of the strain causing
CC the infection allows early, and more specific fungicidal treatment.

SO Sequence 561 BP; 145 A; 152 C; 135 G; 126 T; 3 other;

Query Match 90.5%; Score 19; DB 19; Length 561;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ctacacctgcgaactgga 19
|||||
Db 445 ctacacctgcgaactgga 463

RESULT 5

AAC37182
ID AAC37182 standard; DNA: 510 BP.

XX AAC37182;

DT 17-OCT-2000 (first entry)

XX *Arabidopsis thaliana* DNA fragment SEQ ID NO: 16470.

KM Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

XX *Arabidopsis thaliana*.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 29-MAR-1999; 99US-0126264.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131445.

XX 04-MAY-1999; 99US-0132047.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

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Query Match 81.0%; Score 17; DB 21; Length 510;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 caccctgcgaactggaga 21
|||||
DB 37 caccctgcgaactggaga 53
RESULT 6
AAC45891
ID AAC45891 standard; DNA; 2706 BP.
XX
XX AAC45891;
XX
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 48143.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX EP103405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
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PR 13-OCT-1999: 99US-0159295.
PR 14-OCT-1999: 99US-0159329.
PR 14-OCT-1999: 99US-0159330.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159637.
PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 23-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161820.
PR 28-OCT-1999: 99US-0161892.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.
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Query Match      81.0%; Score 17; DB 21; Length 2706;
Best Local Similarity 100.0%; Pred. No. 41;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 caccctgcgaactgagaga 21
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Db 20 caccctgcgaactgagaga 36
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```
RESULT 7
ABA82622
ID ABA82622 standard; DNA: 33769 BP.
XX
AC ABA82622;
DT 25-JAN-2002 (first entry)
XX
DE Human HBM gene region b527d12-h_contig308G.
XX
```

```
KW Human; high bone mass; HBM gene; zmx1 gene; chromosome 11: 11q13.3;
KW sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW antisense therapy; vaccine; bone disorder; Paget's disease;
KW sclerostosis; osteomalacia; fibrous dysplasia; ds.
```

```
XX Homo sapiens.
XX
XX WO200177327-A1.
XX
XX PD 18-OCT-2001.
XX
XX PF 21-JUN-2000; 2000WO-US16951.
XX
XX PR 05-APR-2000; 2000US-0543771.
XX
XX PR 05-APR-2000; 2000US-0544398.
```

```
XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX PI Carulla JF, Little RD, Recker RR, Johnson ML;
XX
XX DR WPI: 2001-657171/75.
```

```
XX
XX PT New high bone mass (HBM) and zmx1 genes and proteins useful for
XX modulating bone mass for the treatment of e.g. osteoporosis -
XX
XX PS Claim 51; Page 237-257; 443pp; English.
XX
XX
```

```
CC The present invention describes the human zmx1 gene and the high bone
CC mass (HBM) gene, which are found on chromosome 11q13.3. The zmx1 and
CC HBM genes have osteopathic activities. The genes can be used in gene
CC therapy, antisense therapy and in the production of vaccines. They
CC can be used in the diagnosis and treatment of bone disorders including
CC osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous
CC dysplasia. ABA82038 to ABA82760 and AAC68168 to AAC68193 represent
CC sequences used in the exemplification of the present invention.
XX
```

```
SO Sequence 33769 BP; 8178 A; 10222 C; 8617 G; 6749 T; 3 other:
```

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Query Match      77.1%; Score 16.2; DB 22; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 ctaacacctgcgaactgagaga 21
   ||| ||||| ||||| ||
Db 25831 ctagcaccctcgaactgagaga 25851
```

```
RESULT 8
ABL09973
ID ABL09973 standard; cDNA: 1399 BP.
XX
AC ABL09973;
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```
XX
XX DT 26-MAR-2002 (first entry)
```

```

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24401.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PP 23-MAR-2001; 2001WO-US09231.
PR 23-MAR-2000; 2000US-191637P.
PS 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
PA
PI Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
DR P-PSDB; ABB65870.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX Claim 1; SEQ ID NO 24401; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1399 BP; 387 A; 361 C; 338 G; 313 T; 0 other;
SQ
Query Match 75.2%; Score 15.8; DB 23; Length 1399;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 taacacctgcgaactgag 20
1 ||||| ||||| |||||
DB 75 tgacaccgcgaactgag 93

```

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XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
PA
PI Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
DR P-PSDB; ABB58874.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX Claim 1; SEQ ID NO 3413; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1815 BP; 462 A; 488 C; 557 G; 308 T; 0 other;
SQ
Query Match 75.2%; Score 15.8; DB 23; Length 1815;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 aacacctgcgaactgaga 21
1 ||| ||||| ||||| |||||
DB 559 agcacatgcgaactgaga 577

```

```

RESULT 9
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ID ABL02977 standard; cDNA; 1815 BP.
XX
XX ABL02977;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 3413.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF

```

```

RESULT 10
AB109972
ID ABL09972 standard; cDNA; 3399 BP.
XX
XX ABL09972;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24398.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR
DR P-PSDB; ABB65869.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT

```


Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 aacacctgcgaactggaga 21
1 ||||| ||||| ||||| |||||
Db 1559 agcacatcgcaactggaga 1577

RESULT 13

ABL08778 ID ABL08778 standard; cDNA: 4394 BP.

ABL08778; ABL08778;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 20816.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PMD, Myers EW;

WPI: 2001-656860/75.

P-PSDB: ABB64675.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 20816; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins

(AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 4394 BP; 1217 A; 1007 C; 1015 G; 1155 T; 0 other;

Query Match 75.2%; Score 15.8; DB 23; Length 4394;

Best Local Similarity 89.5%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 taacacctgcgaactggag 20

1 ||||| ||||| ||||| |||||

Db 208 tgacaccccgcaactggag 226

RESULT 14

ABL08780 ID ABL08780 standard; cDNA: 4763 BP.

ABL08780; ABL08780;

ABL08780;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 20822.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ss.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PMD, Myers EW;

WPI: 2001-656860/75.

P-PSDB: ABB64677.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

Claim 1; SEQ ID NO 20822; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins

(AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 4763 BP; 1170 A; 1167 C; 1147 G; 1279 T; 0 other;

Query Match 75.2%; Score 15.8; DB 23; Length 4763;

Best Local Similarity 89.5%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 taacacctgcgaactggag 20

1 ||||| ||||| ||||| |||||

Db 4132 tgacaccccgcaactggag 4150

RESULT 15

ABL18503/c ID ABL18503 standard; DNA: 989 BP.

ABL18503; ABL18503;

26-MAR-2002 (first entry)

Drosophila melanogaster genomic polynucleotide SEQ ID NO 6982.

Drosophila: developmental biology; cell signalling; insecticide;

pharmaceutical; gene; ds.

Drosophila melanogaster.

WO200171042-A2.

XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PA
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI: 2001-656860/75.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
PS Claim 1; SEQ ID NO 6982; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU01840-ABU16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 989 BP; 228 A; 245 C; 234 G; 282 T; 0 other;

Query Match 73.3%; Score 15.4; DB 23; Length 989;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 acactcgcaactggag 20
|||||
DB 191 ACACCTCGCACTGGAG 175

Search completed: August 21, 2002, 22:22:51
Job time: 5791 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 21:32:27 ; Search time 5019.06 Seconds
(without alignments)
56.472 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21
Sequence: 1 cttaacctgcgaactggaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gsa:*
13: em_gsa_hum:*
14: em_gsa_huv:*
15: em_gsa_pin:*
16: em_gsa_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	16.8	80.0	362	9	BE070797 RC3-BT050
2	16.8	80.0	458	12	AO681735 HS-2142_A
3	16.8	80.0	552	12	A2191211 SP_1019_A
4	16.8	80.0	610	10	BM440563 pgrin.pk0
5	16.8	80.0	972	12	CNS00777X
6	16.8	80.0	1321	10	BT490849 603031810
7	16.4	78.1	174	9	AT001540
8	16.4	78.1	300	9	AT019460
9	16.4	78.1	376	9	AV191390
10	16.4	78.1	380	10	AV191390
11	16.4	78.1	394	10	BU154339
12	16.4	78.1	469	9	AM582687
13	16.4	78.1	586	9	AU218666
14	16.4	78.1	587	10	BE619904
15	16.4	78.1	713	12	BH064238
16	16.4	78.1	787	12	BH061459
17	16.4	78.1	819	12	BH061403

C 18	16.2	77.1	252	12	A2468148
C 19	16.2	77.1	266	9	AV043034
C 20	16.2	77.1	293	9	BB089128
C 21	16.2	77.1	293	9	BB572305
C 22	16.2	77.1	326	12	A0260963
C 23	16.2	77.1	349	12	A0013861
C 24	16.2	77.1	430	12	A0836420
C 25	16.2	77.1	437	9	AA840330
C 26	16.2	77.1	439	9	AM081834
C 27	16.2	77.1	452	10	BF320988
C 28	16.2	77.1	492	12	A0585499
C 29	16.2	77.1	497	10	M45853
C 30	16.2	77.1	497	12	A0138222
C 31	16.2	77.1	513	9	AA530317
C 32	16.2	77.1	521	9	AM701534
C 33	16.2	77.1	547	9	AL601781
C 34	16.2	77.1	579	12	A2965522
C 35	16.2	77.1	648	12	AG106800
C 36	16.2	77.1	659	9	BE198784
C 37	16.2	77.1	803	10	BG285094
C 38	16.2	77.1	839	10	BG872601
C 39	16.2	77.1	974	10	BI415029
C 40	16.2	77.1	998	10	BG622763
C 41	16.2	77.1	1101	12	CNS000C25
C 42	16.2	77.1	1519	9	AM727720
C 43	16.2	77.1	1559	10	BI160925
C 44	16.2	77.1	1903	11	AK015469
C 45	16.2	77.1	3073	11	AK004854

ALIGNMENTS

RESULT 1
LOCUS BE070797 362 bp mRNA linear EST 09-JUN-2000
DESCRIPTION RC3-BT0502-251199-011-b12 BT0502 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE070797
VERSION BE070797.1 GI:8415443
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eumetazoa; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 362)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.U.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

CONTACT: Simpson A.U.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC3-BT0502-251

199-011-b12&t3=1999-11-25&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 28

High quality sequence stop: 362.

Location/Qualifiers

1..362
/organism="Homo sapiens"

FEATURES

source

/db_xref="taxon:9606"
 /clone_lib="B70502"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ONESTEPS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 82 a 120 c 47 g 113 t
 ORIGIN

Query Match 80.0%; Score 16.8; DB 9; Length 362;
 Best Local Similarity 90.0%; Pred. No. 4.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ctacacctcgcaactgag 20
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 Db 39 CTAACTTCTCGCAACTGAG 58

RESULT 2
 LOCUS AO681735 458 bp DNA linear GSS 28-JUN-1999
 DEFINITION HS_2142_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2142 Col=8 Row=1, DNA sequence.
 ACCESSION AO681735
 VERSION AO681735.1 GI:52527718
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 458)
 Mahairas,G.G., Wallace,J.C., Smith,R., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.husc.washington.edu
 Plate: 2142 row: 1 column: 8
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 458.

FEATURES
 source 1..458
 Location/Qualifiers

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 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
 BASE COUNT 114 a 122 c 106 g 109 t 7 others
 ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 458;
 Best Local Similarity 90.0%; Pred. No. 5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 439 CTAACTTCTCGCAACTGAG 458

RESULT 3
 LOCUS AZ191211 552 bp DNA linear GSS 30-AUG-2000
 DEFINITION SP_1019_A1_A04_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1019 Col=7 Row=A, DNA sequence.
 ACCESSION AZ191211
 VERSION AZ191211.1 GI:8374390
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 552)
 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Blondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
 A sea urchin genome project: Sequence scan, virtual map, and additional resources
 Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 1019 row: A column: 7
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 552.

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
 MEDLINE 20402566
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 1019 row: A column: 7
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 552.

FEATURES
 source 1..552
 Location/Qualifiers

/organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone_lib="Plate=1019 Col=7 Row=A"
 /clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"
 BASE COUNT 173 a 106 c 105 g 164 t 4 others
 ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 552;
 Best Local Similarity 85.7%; Pred. No. 5.3e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ctacacctcgcaactgaga 21
 ||| ||||| ||||| |||||
 Db 407 CTAGCACCCTCGNATCTGAGCA 427

RESULT 4
 LOCUS BM440563 610 bp mRNA linear EST 01-FEB-2002
 DEFINITION pgrih.pk003.h4 Normalized Chicken Reproductive Tract cDNA Library (pgrin) Gallus gallus cDNA clone pgrin.pk003.h4 5' similar to no significant hits (plog(p) 4), mRNA sequence.
 ACCESSION BM440563
 VERSION BM440563.1 GI:18471338
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 80.0%; Score 16.8; DB 12; Length 552;
 Best Local Similarity 85.7%; Pred. No. 5.3e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 610)
 AUTHORS Cogburn, L.A. and Nys, Y.
 TITLE ESTs from Normalized Chicken Reproductive Tract cDNA library-
 University of Delaware and INRA, Tours-Poultry unit Project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburnudel.edu, www.chickest.udel.edu.

FEATURES
 source
 1. 610
 /organism="Gallus gallus"
 /strain="Commercial broiler and layer"
 /db_xref="taxon:9031"
 /clone="pgrln.pk003.h4"
 /clone_lib="Normalized Chicken Reproductive Tract cDNA
 library (pgrln)"
 /sex="Male and Female"
 /tissue_type="Testis, ovary and oviduct"
 /dev_stage="Various stages: embryonic, post-hatch, immature
 and sexually-mature"
 /lab_host="E. coli EMDH10B"
 /note="Vector: PCMVSPORT6; Library made from three total
 RNA pools from each tissue (testis 25%, ovary 25%, and
 oviduct 50% of final RNA pool); Single pass sequencing
 from 5'-end"

BASE COUNT 148 a 145 c 141 g 176 t

ORIGIN

Query Match 80.0%; Score 16.8; DB 10; Length 610;
 Best Local Similarity 90.0%; Pred. No. 5.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 taacacctgcgaactggaga 21
 ||| ||||| ||||| |||||

Db 550 TAAACCTCGCAATGAGAGA 569

RESULT 5
 CENS0777Y 972 bp DNA linear GSS 08-JUL-2001
 LOCUS T7 end of clone BB0AA009H05 of library BB0AA from strain CBS 4732
 DEFINITION of *Pichia angusta*, genomic survey sequence.
 ACCESSION AL432356
 VERSION AL432356.1 GI:12215770
 KEYWORDS GSS.
 SOURCE *Pichia angusta*.
 ORGANISM *Pichia angusta*
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; *Pichia*.
 1 (bases 1 to 972)
 Blandin, G., Florente, B., Malpertuy, A., Wincker, P., Artiguenave, F.
 and Dujon, B.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia*
angusta
 JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
 MEDLINE 20584723
 REFERENCE 2 (bases 1 to 972)
 Soucier, J.L., Algle, M., Artiguenave, F., Blandin, G.,
 Boloitin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
 de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Florente, B.,
 Malpertuy, A., Neveuglise, C., Ozler-Kalogeropoulos, O., Potter, S.,
 Saurin, M., Tekala, F., Toffano-Nioche, C., Wesolowski-Douvet, M.,
 Wincker, P. and Weissbach, J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711

REFERENCE 3 (bases 1 to 972)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen
 yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces*
exiguus, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*,
Saccharomyces kluyveri, *Kluyveromyces thermotolerans*, *Kluyveromyces*
lactis var. *lactis*, *Kluyveromyces marianus* var. *marianus*, *Pichia*
angusta, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*,
Candida tropicalis and *Yarrowia lipolytica*. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

FEATURES
 source
 1. 972
 /organism="Pichia angusta"
 /strain="CBS 4732"
 /db_xref="taxon:4905"
 /clone="BB0AA009H05"
 /clone_lib="BB0AA"
 /note="end : 77"

BASE COUNT 289 a 247 c 236 g 198 t 2 others

ORIGIN

Query Match 80.0%; Score 16.8; DB 12; Length 972;
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 taacacctgcgaactggaga 21
 ||||| ||||| |||||

Db 772 TAAACCTCGCAATGAGAGA 791

RESULT 6
 BI490849 1321 bp mRNA linear EST 28-AUG-2001
 LOCUS 603031810T1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172818 3',
 DEFINITION mRNA sequence.
 ACCESSION BI490849
 VERSION BI490849.1 GI:15330077
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1321)
 NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1430 row: d column: 03
 High quality sequence stop: 749.
 Location/Qualifiers
 1. 1321
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5172818"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MCC Library."

BASE COUNT 363 a 310 c 430 g 218 t

ORIGIN

Query Match 80.0%; Score 16.8; DB 10; Length 1321;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 taacactcgcaactgaga 21
||||| ||||| |||||
Db 1262 TAACACCACGACACGAGA 1281

RESULT 7
AT001540 174 bp mRNA linear EST 26-MAR-1999
LOCUS AT001540 Acanthamoeba healyi CDNA library Acanthamoeba healyi CDNA
DEFINITION clone Ahc507, mRNA sequence.
ACCESSION AT001540
VERSION AT001540.1 GI:4528633
KEYWORDS EST.
SOURCE Acanthamoeba healyi.
ORGANISM Acanthamoeba healyi.
REFERENCE 1 (bases 1 to 174)
AUTHORS Kong,H.H., Hwang,M.Y., Yu,H.S., Hong,Y.C., Kim,T.O. and Chung,D.I.
TITLE New insight into biology of Acanthamoeba healyi by expressed sequence tag analysis
JOURNAL Unpublished (1999)
COMMENT Contact: Kong HH
Department of Parasitology
Kyungpook National University School of Medicine
101 Dongin-dong, Chung-ku, Taegu 700 - 422, Korea
Email: hhkong@h.kyungpook.ac.kr.

FEATURES
source
1. 174
/organism="Acanthamoeba healyi"
/strain="QC-3A"
/db_xref="taxon:65661"
/clone="Ahc507"
/dev_stage="trophozoite"
/clone_lib="Acanthamoeba healyi CDNA library"

BASE COUNT 38 a 52 c 52 g 32 t

ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 174;
Best Local Similarity 94.4%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 aacactcgcaactgaga 21
||| ||||| ||||| |||||
Db 25 ACACCTCGCAACTGAGAGA 42

RESULT 8
AV179460 300 bp mRNA linear EST 21-JUL-1999
LOCUS AV179460/yuji Kohara unpublished CDNA:Strain N2 hermaphrodite
DEFINITION embryo Caenorhabditis elegans CDNA clone yk593d12 3', mRNA
sequence.
ACCESSION AV179460
VERSION AV179460.1 GI:5559361
KEYWORDS EST.
SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 300)
AUTHORS Kohara,Y., Shin-I,Y., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishiyaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk593d12"
/clone_lib="yuji Kohara unpublished CDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 76 a 65 c 71 g 85 t 3 others

ORIGIN

Query Match 78.1%; Score 16.4; DB 9; Length 300;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 aacactcgcaactgag 20
||||| ||||| ||||| |||||
Db 199 AACACTCGCAACTGAG 182

RESULT 9
AV191390 376 bp mRNA linear EST 22-JUL-1999
LOCUS AV191390/yuji Kohara unpublished CDNA:Strain N2 hermaphrodite
DEFINITION embryo Caenorhabditis elegans CDNA clone yk593d12 5', mRNA
sequence.
ACCESSION AV191390
VERSION AV191390.1 GI:5573542
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 376)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishiyaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES
source
1. 376
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk593d12"

clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 117 a 85 c 94 g 80 t

ORIGIN

Query Match 78.1% Score 16.4; DB 10; Length 376;
Best Local Similarity 94.4%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 aacacctcgcaactggag 20
||||| |||||||||

Db 313 AACACTTCGCAACTGAG 330

RESULT 10
BJ154339 380 bp mRNA linear EST 24-JAN-2002
LOCUS BJ154339 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1329g02 3', mRNA sequence.
ACCESSION BJ154339
VERSION BJ154339.1 GI:18322324
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 380)
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 380
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 108 a 72 c 87 g 113 t

ORIGIN

Query Match 78.1% Score 16.4; DB 10; Length 380;
Best Local Similarity 94.4%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 aacacctcgcaactggag 20
||||| |||||||||

Db 255 AACACTTCGCAACTGAG 238

RESULT 11
BJ125969 394 bp mRNA linear EST 23-JAN-2002
LOCUS BJ125969 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1329g02 5', mRNA sequence.
ACCESSION BJ125969
VERSION BJ125969.1 GI:18286116
KEYWORDS EST.

SOURCE
ORGANISM Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 394)
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 394
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 123 a 88 c 72 g 111 t

ORIGIN

Query Match 78.1% Score 16.4; DB 10; Length 394;
Best Local Similarity 94.4%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 aacacctcgcaactggag 20
||||| |||||||||

Db 126 AACACTTCGCAACTGAG 143

RESULT 12
AW582687 469 bp mRNA linear EST 16-MAR-2000
LOCUS RC0-ST0299-070100-011-g06 ST0299 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW582687
ACCESSION AW582687
VERSION AW582687.1 GI:7257736
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 469)
HGCP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC0&c2=RC0-ST0299-
070100-011-g06&c3=2000-01-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 55
High quality sequence stop: 195.
Location/Qualifiers
1. 469
/organism="Homo sapiens"

```

/db_xref="taxon:9606"
/clone_lib="ST0299"
/dev_stage="Adult"
/note="organ: stomach; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      141 a      120 c      123 g      85 t
ORIGIN

Query Match      78.1%; Score 16.4; DB 9; Length 469;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      3 aacacctgcgaactggag 20
        ||||| ||||| |||||
Db      354 AACACTGCAACTGAG 371

RESULT 13
AU218666/c      586 bp      mRNA      linear      EST 17-JUL-2001
LOCATION
DEFINITION      AU218666 unpublished oligo-capped cDNA library, stage L1
                  Caenorhabditis elegans cDNA clone yk867e09 3', mRNA sequence.
ACCESSION      AU218666
VERSION        AU218666.1 GI:14856823
KEYWORDS       EST.
SOURCE         Caenorhabditis elegans.
ORGANISM       Caenorhabditis elegans.
REFERENCE      1 (bases 1 to 586)
AUTHORS        Kohara,Y., Smith,I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
                and Sugano,S.
TITLE          A complementary view of the C.elegans genome
JOURNAL        Unpublished (2001)
COMMENT        Contact: Yuji Kohara
                Genome Biology Lab.
                National Institute of Genetics
                Yata 1111, Mishima, Shizuoka 411, Japan
                Tel: 81-559-81-6854
                Fax: 81-559-81-6855
                Email: ykohara@lab.nig.ac.jp.
FEATURES
  source
    1..586
    /organism="Caenorhabditis elegans"
    /strain="N2"
    /db_xref="taxon:6239"
    /clone="yk867e09"
    /clone_lib="unpublished oligo-capped cDNA library, stage
    L1"
    /sex="Hermaphrodite"
    /tissue_type="whole animal"
    /dev_stage="L1"
BASE COUNT      153 a      126 c      135 g      171 t      1 others
ORIGIN

Query Match      78.1%; Score 16.4; DB 9; Length 586;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      3 aacacctgcgaactggag 20
        ||||| ||||| |||||
Db      247 AACACTGCAACTGAG 230

RESULT 14
BF619904

```

```

LOCUS      BF619904      587 bp      mRNA      linear      EST 22-OCT-2001
DEFINITION      HVSMC0009K02f Hordeum vulgare seedling shoot EST library
                  HVCNMA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
                  HVSMC0009K02f, mRNA sequence.
ACCESSION      BF619904
VERSION        BF619904.2 GI:13107889
KEYWORDS
SOURCE         barley.
ORGANISM       Hordeum vulgare
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
                ; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 587)
AUTHORS        Wing,R., Close,T.J., Kleinofe,A., Wise,R., Begum,D., Fritsch,D., Yu
                ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chol,D.W., Fenton
                ,R.D., Oates,R. and Main,D.
TITLE          Development of a genetically and physically anchored EST resource
                for barley genomics: Morex unstressed seedling shoot cDNA library
                Unpublished (2001)
COMMENT        On Dec 18, 2000 this sequence version replaced gi:11883638.
                Contact: Wing RA
                Clemson University Genomics Institute
                Clemson University
                100 Jordan Hall, Clemson, SC 29634, USA
                Tel: 864 656 7288
                Fax: 864 656 4293
                Email: rwing@clemson.edu
                Total hg bases = 393
                Seq primer: AATTAACTCCTCACTAAGGC
                High quality sequence stop: 576.
FEATURES
  source
    1..587
    /organism="Hordeum vulgare"
    /cultivar="Morex"
    /db_xref="taxon:4513"
    /clone="HVSMC0009K02f"
    /clone_lib="Hordeum vulgare seedling shoot EST library
    HVCNMA0003 (Etiolated and unstressed)"
    /tissue_type="Seedling shoot"
    /lab_host="TJC121"
    /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
    Seeds were surface sterilized then germinated under axenic
    conditions in the dark at room temperature on filter paper
    with water, nystatin and cefotaxime in covered
    crystallization dishes. Five-day old seedling shoots were
    then harvested, total RNA was prepared, poly(A) RNA was
    purified, one primary unamplified cDNA library was made,
    and 1 million pfu were in vivo excised to give pluescript
    SK(-) cDNA phagemids. These steps were performed in the TJ
    Close laboratory at the University of California,
    Riverside (Choi, Close, Fenton). Phagemids were plated and
    picked at the Clemson University Genomics Institute (CUGI)
    (Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA
    preparations, DNA sequencing and sequence analysis were
    performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
    , Rambo, Main). The sequence has been trimmed to remove
    vector sequence and contains a minimum of 100 bases of
    phred value 20 or above. For more details on library
    preparation and sequence analysis see
    http://www.genome.clemson.edu/projects/barley. To order
    this clone see http://www.genome.clemson.edu/orders Also
    see Close TJ, Wing R, Kleinofe A, Wise R (2001)
    Genetically and physically anchored EST resources for
    barley genomics. Barley Genetics Newsletter 31:29-30.
    (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      163 a      117 c      171 g      136 t
ORIGIN

Query Match      78.1%; Score 16.4; DB 10; Length 587;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 3 aacctgcgaactggag 20
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 Db 96 AACACCTGCTACTGGAG 113

RESULT 15

BH064238 713 bp DNA linear GSS 18-JUL-2001
 LOCUS BH064238/c
 DEFINITION RPI-24-370K21.TV RPI-24 Mus musculus genomic clone RPI-24-370K21
 , DNA sequence.
 ACCESSION BH064238
 VERSION BH064238.1 GI:14879771
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
 Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
 Russell,D., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPI-24
 Unpublished (1999)
 Other GSSs: RPI-24-370K21.TJ

TITLE
 JOURNAL
 COMMENT
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhaod@tigr.org

Clones are derived from the mouse BAC library RPI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@email.cho.org). Clones may be purchased from BACPAC
 Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 370 row: K column: 21
 Seq primer: 77
 Class: BAC ends.

FEATURES

source Location/Qualifiers
 1..713
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPI-24-370K21"
 /clone_id="RPI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTARBAC1. Site 1: BamHI. Site 2: BamHI.
 RPI-24 Mouse BAC Library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

BASE COUNT 170 a 157 c 175 g 211 t
 ORIGIN

Query Match 78.1%; Score 16.4; DB 12; Length 713;
 Best Local Similarity 94.4%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 aacctgcgaactggaga 21
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 Db 463 ACACCTGCACTGGAGA 446

Search completed: August 21, 2002, 21:32:34
 Job time: 12533 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:12:32 ; Search time 138.45 Seconds
(without alignments)
37.238 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21

Sequence: 1 ctaccactcgcactcgtgaga 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	90.5	561	1 US-08-905-314A-24	Sequence 24, Appl
2	14.6	69.5	517	4 US-09-276-531-122	Sequence 122, App
3	14.6	69.5	1766	5 PCT-US93-00601-1	Sequence 1, Appl1
4	14.6	69.5	1766	5 PCT-US94-07107A-1	Sequence 1, Appl1
5	14.6	69.5	1767	4 US-08-083-945C-1	Sequence 1, Appl1
6	14.6	69.5	1784	1 US-08-554-612C-13	Sequence 13, Appl1
7	14.6	69.5	2636	1 US-08-554-612C-12	Sequence 12, Appl1
8	14.6	69.5	2898	1 US-08-554-612C-51	Sequence 51, Appl1
9	14.6	69.5	2909	1 US-08-554-612C-10	Sequence 10, Appl1
10	14.6	69.5	2909	1 US-08-554-612C-11	Sequence 11, Appl1
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15	14.2	67.6	2434	4 US-09-272-496-1	Sequence 1, Appl1
16	14.2	67.6	2601	4 US-08-569-749-3	Sequence 3, Appl1
17	14.2	67.6	2601	5 PCT-US96-12860-3	Sequence 3, Appl1
18	14.2	67.6	2676	2 US-08-511-485-5	Sequence 5, Appl1
19	14.2	67.6	3076	2 US-09-205-144-1	Sequence 1, Appl1
20	14.2	67.6	3416	2 US-08-724-394A-15	Sequence 15, Appl1
21	14.2	67.6	3463	2 US-09-189-462-3	Sequence 3, Appl1
22	14.2	67.6	4131	1 US-08-485-588-4	Sequence 4, Appl1
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24	14.2	67.6	4131	2 US-08-480-751-4	Sequence 4, Appl1
25	14.2	67.6	4131	2 US-08-943-986-4	Sequence 4, Appl1
26	14.2	67.6	4131	3 US-08-353-784-4	Sequence 4, Appl1
27	14.2	67.6	4131	3 US-08-484-719B-4	Sequence 4, Appl1

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c	33	14.2	67.6	5115	3 US-08-476-509B-3	Sequence 3, Appl1
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c	36	14.2	67.6	6669	4 US-09-617-053A-5	Sequence 5, Appl1
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c	38	13.8	65.7	525	3 US-08-911-853-18	Sequence 18, Appl1
c	39	13.8	65.7	525	4 US-09-479-409-18	Sequence 18, Appl1
c	40	13.8	65.7	525	4 US-09-479-453-18	Sequence 18, Appl1
c	41	13.8	65.7	780	1 US-08-325-553-27	Sequence 27, Appl1
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c	43	13.8	65.7	2272	1 US-08-482-577B-1	Sequence 1, Appl1
c	44	13.8	65.7	2272	3 US-08-289-222E-2	Sequence 2, Appl1
c	45	13.8	65.7	2272	4 US-09-218-176-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-905-314A-24
Sequence 24, Application US/08905314A
Patent No. 5827695
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5827695artis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Fusarium avenaceum
INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note="3' end of small subunit
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NAME/KEY: misc_feature
LOCATION: 31..181

OTHER INFORMATION: /note="ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 182..338
OTHER INFORMATION: /note="5.8S rRNA gene"
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LOCATION: 339..504
OTHER INFORMATION: /note="ITS 2"
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LOCATION: 505..561
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US-08-905-314A-24

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Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 19
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DB 445 CTAACACCTCGCAACTGGA 463

RESULT 2
US-09-276-531-122
Sequence 122, Application US/09276531
Patent No. 6183968
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
NUMBER OF SEQUENCES: 134
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murty, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNG0708
CLONE: 2642108
US-09-276-531-122

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Best Local Similarity 81.0%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 442 CTAACACTTGTACTGAGGA 462

RESULT 3
PCT-US93-00601-1
Sequence 1, Application PC/TUS9300601
GENERAL INFORMATION:
APPLICANT: Becker, Marie E.
APPLICANT: Liotta, Lance A.
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00601
FILING DATE: 19930129
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1766 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 35..1279
PCT-US93-00601-1

Query Match 69.5%; Score 14.6; DB 5; Length 1766;
Best Local Similarity 81.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 ctacacctcgcaactgaga 21
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DB 66 CTGACACCCCGCCTGAGGA 86

RESULT 4
PCT-US94-07107A-1
Sequence 1, Application PC/TUS9407107A
GENERAL INFORMATION:
APPLICANT: The Government of the United States of
APPLICANT: America, as represented by the Secretary,
Department of Health and Human Services
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 15

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Query Match 69.5%; Score 14.6; DB 1; Length 1784;
Best Local Similarity 81.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctaacactcgcaactggaga 21
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Db 1099 CTAACATCTCGCACCAGTAGA 1079

RESULT 7

US-08-554-612C-12/C
Sequence 12, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:
APPLICANT: Orllicky, David
TITLE OF INVENTION: PROSTAGLANDIN F2₁ RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660emder 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-554-612C-12

Query Match 69.5%; Score 14.6; DB 1; Length 2636;
Best Local Similarity 81.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctaacactcgcaactggaga 21
||||| ||||| |||||
Db 1099 CTAACATCTCGCACCAGTAGA 1079

RESULT 8

US-08-554-612C-51/C
Sequence 51, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:
APPLICANT: Orllicky, David
TITLE OF INVENTION: PROSTAGLANDIN F2₁ RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660emder 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-554-612C-51

Query Match 69.5%; Score 14.6; DB 1; Length 2898;
Best Local Similarity 81.0%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ctaacactcgcaactggaga 21
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Db 1088 CTAACATCTCGCACCAGTAGA 1068

RESULT 9

US-08-554-612C-10/C
Sequence 10, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:
APPLICANT: Orllicky, David
TITLE OF INVENTION: PROSTAGLANDIN F2₁ RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660emder 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-10

Query Match 69.5%; Score 14.6; DB 1; Length 2909;
Best Local Similarity 81.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ctaacacctgcgaactggaga 21
||||| ||||| ||||| |||||
Db 1099 ctaacacctgcgaactggaga 1079

RESULT 10
US-08-554-612C-11/C
Sequence 11, Application US/08554612C
Patent No. 5747660

GENERAL INFORMATION:
APPLICANT: Orlicky, David
TITLE OF INVENTION: PROSTAGLANDIN F₂ RECEPTOR REGULATORY
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-11

Query Match 69.5%; Score 14.6; DB 1; Length 2909;
Best Local Similarity 81.0%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ctaacacctgcgaactggaga 21
||||| ||||| ||||| |||||
Db 1099 ctaacacctgcgaactggaga 1079

RESULT 11
US-08-554-612C-2/C
Sequence 2, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:

APPLICANT: Orlicky, David
TITLE OF INVENTION: PROSTAGLANDIN F₂ RECEPTOR REGULATORY
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-2

Query Match 69.5%; Score 14.6; DB 1; Length 5843;
Best Local Similarity 81.0%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ctaacacctgcgaactggaga 21
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Db 1137 ctaacacctgcgaactggaga 1117

RESULT 12
US-09-386-493-9
Sequence 9, Application US/09386493
Patent No. 6262247

GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
APPLICANT: Azimzal, Yalda
TITLE OF INVENTION: POLYCYCLIC AROMATIC HYDROCARBON INDUCED MOLECULES
FILE REFERENCE: PB-0011 US
CURRENT APPLICATION NUMBER: US/09/386,493
CURRENT FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 9

LENGTH: 644
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: unsure
LOCATION: 44
OTHER INFORMATION: a or g or c or t, unknown, or other
FEATURE:
NAME/KEY:
OTHER INFORMATION: 700062690
PUBLICATION INFORMATION:
US-09-386-493-9

Query Match 67.6%; Score 14.2; DB 4; Length 644;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 taacacctgcgaactgag 20
||||| ||| |||||

Db 176 taacacatgcgacatgag 194

RESULT 13

US-08-928-383B-3/C
; Sequence 3, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Flinberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Cocksacklevirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928.383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
; US-08-928-383B-3

Query Match 67.6%; Score 14.2; DB 4; Length 1095;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 taacacctgcgaactgag 20
||||| ||||| ||| ||

Db 440 TAACATCTCGCACCTGAG 422

RESULT 14
US-08-928-383B-1/C
; Sequence 1, Application US/08928383B
; Patent No. 6210921

; GENERAL INFORMATION:
; APPLICANT: Robert W. Flinberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Cocksacklevirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928.383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 60..1157
; US-08-928-383B-1

Query Match 67.6%; Score 14.2; DB 4; Length 1584;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 taacacctgcgaactgag 20
||||| ||||| ||| ||

Db 499 TAACATCTCGCACCTGAG 481

RESULT 15
US-09-272-496-1/C
; Sequence 1, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: Degregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272.496
; EARLIER APPLICATION NUMBER: 1999-03-19
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

: NAME/KEY: CDS
: LOCATION: (60)..(1154)
US-09-272-496-1

Query Match 67.68; Score 14.2; DB 4; Length 2434;
Best Local Similarly 84.2%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 taacacctgcgactggag 20
|||||
Db 499 TAACATCTGCACCTGAAG 481

Search completed: August 21, 2002, 22:12:34
Job time: 5707 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:40 ; Search time 8184.59 Seconds
(without alignments)
55.511 Million cell updates/sec

Title: US-10-046-955-51

Perfect score: 21
Sequence: 1 ctacacctgcgaactgaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	21	100.0	21	US-09-423-233-51	Sequence 51, Appl
2	21	100.0	319	US-09-423-233-6	Sequence 6, Appl
3	19.4	92.4	563	US-09-580-797-10	Sequence 10, Appl
4	19	90.5	561	US-08-905-314-24	Sequence 24, Appl
5	17	81.0	90698	US-09-803-736-1210	Sequence 1210, Appl
6	17	81.0	90698	US-09-803-736-1210	Sequence 1210, Appl
7	17	81.0	141753	US-09-692-412-28	Sequence 28, Appl
8	17	81.0	141753	US-09-803-736-1008	Sequence 1008, Appl
9	16.8	80.0	445	US-09-654-617-4875	Sequence 4875, Appl
10	16.8	80.0	445	US-09-684-016-4875	Sequence 4875, Appl
11	16.2	77.1	313	US-09-205-070-39950	Sequence 39950, A
12	16.2	77.1	313	US-09-321-214-6054	Sequence 6054, A
13	16.2	77.1	313	US-09-340-623-39950	Sequence 39950, A
14	16.2	77.1	313	US-09-516-335-6054	Sequence 6054, A
15	16.2	77.1	313	US-09-733-811-6054	Sequence 6054, A
16	16.2	77.1	313	US-09-798-888-39950	Sequence 39950, A
17	16.2	77.1	313	US-09-898-888A-39950	Sequence 6054, A
18	16.2	77.1	313	US-09-975-640-6054	Sequence 6054, A
19	16.2	77.1	313	US-09-975-640A-6054	Sequence 6054, A
20	16.2	77.1	313	US-09-975-640A-6054	Sequence 1212, A
21	16.2	77.1	313	US-09-289-768-12122	Sequence 1212, A
22	16.2	77.1	313	US-09-939-397-12122	Sequence 6054, A
23	16.2	77.1	313	US-09-252-833-602	Sequence 55728, A
24	16.2	77.1	380	US-09-521-640-55728	Sequence 55728, A
25	16.2	77.1	403	US-09-874-708A-59772	Sequence 59772, A
26	16.2	77.1	403	US-60-211-725-58685	Sequence 58685, A
27	16.2	77.1	427	US-09-293-972-29952	Sequence 29952, A
28	16.2	77.1	427	US-09-904-939-29952	Sequence 29952, A
29	16.2	77.1	427	US-60-360-207-25416	Sequence 25416, A
30	16.2	77.1	489	US-09-606-977-60445	Sequence 60445, A
31	16.2	77.1	499	US-09-634-306B-136133	Sequence 136133, A

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32 16.2 77.1 499 24 US-09-634-306B-136134 Sequence 136134,
c 33 16.2 77.1 599 28 US-09-702-134-38705 Sequence 38705, A
34 16.2 77.1 599 31 US-09-815-264-100800 Sequence 100800,
35 16.2 77.1 745 56 US-60-172-362-3540 Sequence 3540, Ap
36 16.2 77.1 1037 24 US-09-634-306B-259445 Sequence 259445,
37 16.2 77.1 1037 24 US-09-634-306B-259446 Sequence 259446,
38 16.2 77.1 1037 24 US-09-634-306B-259447 Sequence 259447,
39 16.2 77.1 1234 25 US-09-652-125A-9371 Sequence 9371, Ap
40 16.2 77.1 1237 19 US-09-522-303-1121 Sequence 1121, Ap
41 16.2 77.1 1493 24 US-09-620-392-1714 Sequence 1714, Ap
42 16.2 77.1 4005 64 US-60-238-273-228 Sequence 228, App
43 16.2 77.1 4343 24 US-09-620-392-17241 Sequence 17241, A
44 16.2 77.1 12260 24 US-09-620-392-17242 Sequence 17242, A
45 16.2 77.1 12792 62 US-60-230-435-71 Sequence 71, Appl
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ALIGNMENTS

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RESULT 1
US-09-423-233-51
; Sequence 51, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-51
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Query Match 100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ctacacctgcgaactggaga 21
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RESULT 2
US-09-423-233-6
; Sequence 6, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341WP
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Fusarium solani
US-09-423-233-6
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Query Match 100.0%; Score 21; DB 18; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ctacacctgcgaactggaga 21
Db 222 ctacacctgcgaactggaga 242
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RESULT 3
US-09-580-797-10
; Sequence 10, Application US/09580797
; GENERAL INFORMATION:
```

```
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; APPLICANT: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Fusarium solani
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: n = a or c or g or t
US-09-580-797-10
```

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Query Match 92.4%; Score 19.4; DB 22; Length 563;
Best Local Similarity 93.2%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 ctacacctgcgaactggaga 21
Db 478 ctacacctgcgaactggaga 498
|||||
```

```
RESULT 4
US-08-905-314-24
; Sequence 24, Application US/08905314
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Novartis Corporation Patent Department
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 20779-2257
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,314
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CCC 1944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```



```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Fusarium avenaceum
; INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /note="3' end of small subunit"
;
; OTHER INFORMATION: rRNA gene"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..181
; OTHER INFORMATION: /note="ITS 1"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 182..338
; OTHER INFORMATION: /note="5.8S rRNA gene"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 339..504
; OTHER INFORMATION: /note="ITS 2"
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 505..561
; OTHER INFORMATION: /note="5' end of large subunit"
;
; OTHER INFORMATION: rRNA gene"
;
US-08-905-314-24
```

```

Query Match          90.5%; Score 19; DB 13; Length 561;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 ctacactgcgaactgga 19
    ||||||||||||||||
DB 445 CTACACTGCACACTGGA 463
```

```

RESULT 5
US-09-803-736-1210
; Sequence 1210, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Morris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1582
;
; SEQ ID NO 1210
; LENGTH: 90698
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1210
```

```

Query Match          81.0%; Score 17; DB 31; Length 90698;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 cactcgcgaactgaga 21
    ||||||||||||||||
DB 77736 cactcgcgaactgaga 77752
```

```

RESULT 6
US-09-803-736-1210/c
; Sequence 1210, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Morris, Susan R.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 1582
;
; SEQ ID NO 1210
; LENGTH: 90698
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1210
```

```

Query Match          81.0%; Score 17; DB 31; Length 90698;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 cactcgcgaactgaga 21
    ||||||||||||||||
DB 88914 CACTCGCAACTGAGA 88898
```

```

RESULT 7
US-09-692-412-28
; Sequence 28, Application US/09692412
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)C
; CURRENT APPLICATION NUMBER: US/09/692,412
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 124
;
; SEQ ID NO 28
; LENGTH: 141753
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: unsure
; LOCATION: (1)..(141753)
; OTHER INFORMATION: unsure at all n locations
US-09-692-412-28
```

```

Query Match          81.0%; Score 17; DB 27; Length 141753;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 cactcgcgaactgaga 21
    ||||||||||||||||
DB 138449 cactcgcgaactgaga 138465
```

```

RESULT 8
US-09-803-736-1008
; Sequence 1008, Application US/09803736
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Levin, Irena M.
; APPLICANT: Morris, Susan R.
```

```
; APPLICANT: Rounsley, Steven D.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)D
; CURRENT APPLICATION NUMBER: US/09/803,736
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: Identified by Attorney Docket number 04983.0206CPUS01 38-10
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 1582
; SEQ ID NO 1008
; LENGTH: 141753
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(141753)
; OTHER INFORMATION: unsure at all n locations
US-09-803-736-1008
```

```
Query Match      81.0%; Score 17; DB 31; Length 141753;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      5 caccctgcgaactggaga 21
Db 138449 caccctgcgaactggaga 138465
```

```
RESULT      9
US-09-654-617-4875
; Sequence 4875, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 4875
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Glycine max
US-09-654-617-4875
```

```
Query Match      80.0%; Score 16.8; DB 25; Length 445;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 taacacctgcgaactggaga 21
Db      1 taacacctgcgaactggaga 20
```

```
RESULT     10
US-09-684-016-4875
; Sequence 4875, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 4875
; LENGTH: 445
```

```
; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-4875
```

```
Query Match      80.0%; Score 16.8; DB 27; Length 445;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      2 taacacctgcgaactggaga 21
Db      1 taacacctgcgaactggaga 20
```

```
RESULT     11
US-09-205-070-39950
; Sequence 39950, Application US/09205070
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748
; CURRENT APPLICATION NUMBER: US/09/205,070
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39950
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(313)
; OTHER INFORMATION: n = A,T,C or G
US-09-205-070-39950
```

```
Query Match      77.1%; Score 16.2; DB 16; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 ctacacctgcgaactggaga 21
Db      49 ctacacctgcgaactggaga 69
```

```
RESULT     12
US-09-321-214-6054
; Sequence 6054, Application US/09321214
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Ford, John
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-740
; CURRENT APPLICATION NUMBER: US/09/321,214
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: US 60/088,041
; EARLIER FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6054
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-321-214-6054
```

```
Query Match      77.1%; Score 16.2; DB 17; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ctacactcgcactgaga 21
    ||||| ||||| ||||| |||||
Db 49 ctactctctccactgaga 69

RESULT 13
US-09-340-623-39950
; Sequence 39950, Application US/09340623
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/340,623
; EARLIER FILING DATE: 1999-06-28
; EARLIER APPLICATION NUMBER: US 09/205,070
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39950
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(313)
; OTHER INFORMATION: n = A,T,C or G
US-09-340-623-39950

Query Match      77.1%; Score 16.2; DB 17; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ctacactcgcactgaga 21
    ||||| ||||| ||||| |||||
Db 49 ctactctctccactgaga 69

RESULT 14
US-09-516-335-6054
; Sequence 6054, Application US/09516335
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroja, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Wu, James
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/516,335
; EARLIER FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 60/088,041
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6054
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-516-335-6054
```

```
APPLICANT: Ralsi, Fariba
APPLICANT: Randhwa, Gurpreet
APPLICANT: Sidhu, Navjwan
APPLICANT: Smith, Benjamin
APPLICANT: Smythe, Ashleigh
APPLICANT: Tkach, Joe
APPLICANT: Tran, Lien
APPLICANT: Verna, Ron
APPLICANT: Wachter, Adam
APPLICANT: Wu, James
APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 740CIP
; CURRENT APPLICATION NUMBER: US/09/516,335
; EARLIER FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 09/321,214
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 60/088,041
; NUMBER OF SEQ ID NOS: 31906
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6054
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-516-335-6054

Query Match      77.1%; Score 16.2; DB 19; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ctacactcgcactgaga 21
    ||||| ||||| ||||| |||||
Db 49 ctactctctccactgaga 69

RESULT 15
US-09-733-811-6054
; Sequence 6054, Application US/09733811
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jessen, Aaron
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroja, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nelken, Sarah
; APPLICANT: Nguyen, Kody
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Ralsi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
```

;; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
;; FILE REFERENCE: 740CIP
;; CURRENT APPLICATION NUMBER: US/09/733,811
;; CURRENT FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 09/321,214
;; PRIOR FILING DATE: 1999-05-26
;; PRIOR APPLICATION NUMBER: 60/088,041
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 31906
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6054
;; LENGTH: 313
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-733-811-6054

Query Match 77.1%; Score 16.2; DB 29; Length 313;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctacacctgcgaactggaga 21
||||| ||||| ||||| |||||
Db 49 ctactcctcccccaactggaga 69

Search completed: August 22, 2002, 00:39:53
Job time: 13078 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:57 ; Search time 663.62 seconds
(without alignments)
85.144 Million cell updates/sec

Title: US-10-046-955-51

Sequence: 1 ctacacctgcgaactgaga 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1721111 seqs, 145317543 residues
Total number of hits satisfying chosen parameters: 3442222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-10-046-955-51	Sequence 51, Appl
2	21	100.0	319	US-10-046-955-6	Sequence 6, Appl
3	17	81.0	510	US-09-620-393B-5270	Sequence 5270, Ap
4	16.2	77.1	499	US-10-027-632-136133	Sequence 136133,
5	16.2	77.1	499	US-10-027-632-136134	Sequence 136134,
6	16.2	77.1	1037	US-10-027-632-259445	Sequence 259445,
7	16.2	77.1	1037	US-10-027-632-259446	Sequence 259446,
8	16.2	77.1	1037	US-10-027-632-259447	Sequence 259447,
9	16.2	77.1	33769	PCT-US02-15982-8	Sequence 8, Appl
10	16.2	77.1	33769	US-09-544-398A-8	Sequence 8, Appl
11	16.2	77.1	33769	US-09-544-398B-8	Sequence 8, Appl
12	15.8	75.2	341	US-09-360-039-29617	Sequence 29617, A
13	15.2	72.4	294	US-09-540-210B-34637	Sequence 34637, A
14	15.2	72.4	598	US-10-027-632-224405	Sequence 224405,
15	15.2	72.4	723	US-10-027-632-20739	Sequence 20739, A
16	15.2	72.4	792	US-10-027-632-137644	Sequence 137644,
17	15.2	72.4	792	US-10-027-632-137645	Sequence 137645,
18	15.2	72.4	856	US-10-155-881-37126	Sequence 37126, A
19	15.2	72.4	884	US-10-098-754-14341	Sequence 14341, A
20	15.2	72.4	1244	US-09-886-492-14875	Sequence 14875, A
21	15.2	72.4	1932	US-09-665-308D-17	Sequence 17, Appl
22	15.2	72.4	2685	US-09-935-625-16439	Sequence 16439, A
23	15.2	72.4	2685	US-09-935-625-24778	Sequence 24778, A
24	15.2	72.4	2712	US-09-935-625-9769	Sequence 9769, Ap
25	15.2	72.4	2712	US-09-935-625-26473	Sequence 26473, A

26	15.2	72.4	2757	5	US-09-935-625-10050	Sequence 10050, A
27	15.2	72.4	2757	5	US-09-935-625-26637	Sequence 26637, A
28	15.2	72.4	11485	6	US-10-205-219-144	Sequence 144, Ap
29	14.8	70.5	209	5	US-09-886-492-7487	Sequence 7487, Ap
30	14.8	70.5	258	5	US-09-975-254-27983	Sequence 27983, A
31	14.8	70.5	316	5	US-09-540-210B-34924	Sequence 34924, A
32	14.8	70.5	332	5	US-09-698-495-425	Sequence 425, Ap
33	14.8	70.5	422	5	US-09-886-492-1043	Sequence 1043, Ap
34	14.8	70.5	478	5	US-10-011-154-1257	Sequence 1257, Ap
35	14.8	70.5	478	5	US-09-918-995-11316	Sequence 11316, A
36	14.8	70.5	571	7	US-10-027-632-22591	Sequence 22591, A
37	14.8	70.5	571	7	US-10-027-632-22592	Sequence 22592, A
38	14.8	70.5	571	7	US-10-027-632-22593	Sequence 22593, A
39	14.8	70.5	586	5	US-09-886-492-15318	Sequence 15318, A
40	14.8	70.5	800	7	US-10-027-632-170361	Sequence 170361, A
41	14.8	70.5	906	6	US-10-098-754-11987	Sequence 11987, A
42	14.8	70.5	1161	7	US-10-155-881-35934	Sequence 35934, A
43	14.8	70.5	1155	7	US-10-155-881-35795	Sequence 35795, A
44	14.8	70.5	1214	7	US-10-155-881-14652	Sequence 14652, A
45	14.8	70.5	1372	7	US-10-155-881-14650	Sequence 14650, A

ALIGNMENTS

RESULT 1
US-10-046-955-51
Sequence 51, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 21
TYPE: DNA
ORGANISM: Fusarium solani
US-10-046-955-51

Query Match 100.0% Score 21: DB 7: Length 21:
Best Local Similarity 100.0% Pred. No. 0.15:
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ctacacctgcgaactgaga 21
Db 1 ctacacctgcgaactgaga 21

RESULT 2
US-10-046-955-6
Sequence 6, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.

```
APPLICANT: Reiss, Errol
APPLICANT: Aldorevich, Liliiana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 319
TYPE: DNA
ORGANISM: Fusarium solani
US-10-046-955-6
```

```
Query Match          100.0%; Score 21; DB 7; Length 319;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 ctacacctcgcaactgaga 21
    ||||| ||||| ||||| |||||
DB 222 ctacacctcgcaactgaga 242
```

```
RESULT 3
US-09-620-393B-5270
; Sequence 5270, Application US/09620393B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1066P
; CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5270
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..510
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; NAME/KEY: misc-feature
; LOCATION: 1..510
; OTHER INFORMATION: Ceres Seq. ID 1390380
US-09-620-393B-5270
```

```
Query Match          81.0%; Score 17; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 5 caccctgcactgaga 21
    ||||| ||||| ||||| |||||
DB 37 caccctgcactgaga 53
```

```
RESULT 4
US-10-027-632-136133
; Sequence 136133, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136133
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136133
```

```
Query Match          77.1%; Score 16.2; DB 7; Length 499;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 ctacacctcgcaactgaga 21
    ||||| ||||| ||||| |||||
DB 55 ctacacctcgcaactgaga 75
```

```
RESULT 5
US-10-027-632-136134
; Sequence 136134, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136134
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136134
```

```
Query Match          77.1%; Score 16.2; DB 7; Length 499;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 1 ctacacctgcgaactgagaga 21
||||| ||||| ||||| |||||
Db 55 ctactcctcccccactgagaga 75

RESULT 6
US-10-027-632-259445

; Sequence 259445, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259445
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259445

Query Match 77.1%; Score 16.2; DB 7; Length 1037;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgagaga 21
||||| ||||| ||||| |||||
Db 496 ctacccctgcgaactgagaga 516

RESULT 7
US-10-027-632-259446

; Sequence 259446, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259446
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259446

Query Match 77.1%; Score 16.2; DB 7; Length 1037;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgagaga 21
||||| ||||| ||||| |||||
Db 496 ctacccctgcgaactgagaga 516

RESULT 8
US-10-027-632-259447

; Sequence 259447, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259447
; LENGTH: 1037
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-259447

Query Match 77.1%; Score 16.2; DB 7; Length 1037;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactgagaga 21
||||| ||||| ||||| |||||
Db 496 ctacccctgcgaactgagaga 516

RESULT 9
PCT-US02-15982-8

; Sequence 8, Application PC/TUS0215982
; GENERAL INFORMATION:
; APPLICANT: Allen, Kristina M.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Bhat, Bheem
; APPLICANT: Damagnez, Veronique
; APPLICANT: Robinson, John
; APPLICANT: Jaworsky, Paul
; TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
; FILE REFERENCE: 03796-132
; CURRENT APPLICATION NUMBER: PCT/US02/15982
; CURRENT FILING DATE: 2002-05-17

```
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739),(33749),(33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
PCT-US02-15982-8

Query Match      77.1%; Score 16.2; DB 1; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ctaacacctgcgaactgagaga 21
      ||| ||||| ||||| |||

Db 25831 ctacgacctctcaactgagaca 25851

RESULT 10
; Sequence 8, Application US/09544398A
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739),(33749),(33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-544-398A-8

Query Match      77.1%; Score 16.2; DB 5; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ctaacacctgcgaactgagaga 21
      ||| ||||| ||||| |||

Db 25831 ctacgacctctcaactgagaca 25851

RESULT 11
; Sequence 8, Application US/09544398B
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 33769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (33739),(33749),(33758)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are u
US-09-544-398B-8

Query Match      77.1%; Score 16.2; DB 5; Length 33769;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 ctaacacctgcgaactgagaga 21
      ||| ||||| ||||| |||

Db 25831 ctacgacctctcaactgagaca 25851

RESULT 12
; Sequence 29617/c
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 29617
; LENGTH: 341
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; US-60-360-039-29617

Query Match      75.2%; Score 15.8; DB 8; Length 341;
Best Local Similarity 89.5%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 aacacctgcgaactgagaga 21
      ||||| ||||| ||||| |||

Db 71 AACACCTTGCAACTGGAAA 53

RESULT 13
; Sequence 34637, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
```


APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
PRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: February 27, 1995
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: September 29, 1995
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR FILING DATE: March 25, 1997
PRIOR APPLICATION NUMBER: 60/014,010
PRIOR FILING DATE: March 25, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/803,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,569
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998

PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35634
SOFTWARE: PERL Program
SEQ ID NO 34637
LENGTH: 294
TYPE: DNA
ORGANISM: Rattus norvegicus
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: rat00084384
US-09-540-210B-34637

Query Match 72.4%; Score 15.2; DB 5; Length 294;
Best Local Similarity 85.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 taacacctgcgaactgaga 21
|| ||||| || |||||
Db 17 tatcaactcccaactgaga 36

RESULT 14
US-10-027-632-224405
; Sequence 224405, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224405
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-224405

Query Match 72.4%: Score 15.2; DB 7; Length 598;
Best Local Similarity 85.0%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactggag 20
||| ||||| ||||| |||||
Db 7 ctacacctgcgaactggag 26

RESULT 15

US-10-027-632-20739

; Sequence 20739, Application us/10027632

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20739

; LENGTH: 723

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-20739

Query Match 72.4%: Score 15.2; DB 7; Length 723;
Best Local Similarity 85.0%: Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ctacacctgcgaactggag 20
||| ||||| ||||| |||||
Db 646 ctgacacctggaatggag 665

Search completed: August 22, 2002, 00:51:01
Job time: 11901 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:26 ; Search time 8184.59 Seconds

(Without alignments)
843.235 Million cell updates/sec

Title: US-10-046-955-6

Perfect score: 319

Sequence: 1 gaatacgataagtaagt.....ggataccgcgtgaactta 319

Scoring table: IDENTITY_NIC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/1/pna/PCRTUS.COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06.COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07.COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08.COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US081.COMB.seq.*
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23: /cgn2_6/ptodata/1/pna/US096A.COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US096B.COMB.seq.*
25: /cgn2_6/ptodata/1/pna/US096C.COMB.seq.*
26: /cgn2_6/ptodata/1/pna/US096D.COMB.seq.*
27: /cgn2_6/ptodata/1/pna/US096E.COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US097A.COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US097B.COMB.seq.*
30: /cgn2_6/ptodata/1/pna/US097C.COMB.seq.*
31: /cgn2_6/ptodata/1/pna/US098A.COMB.seq.*
32: /cgn2_6/ptodata/1/pna/US098B.COMB.seq.*
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43: /cgn2_6/ptodata/1/pna/US6004.COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	319	100.0	319	18	US-09-423-233-6
2	241.4	75.7	563	22	US-09-580-797-10
3	240.4	75.4	534	36	US-09-961-755A-7
4	240.2	75.3	310	18	US-09-423-233-7
5	240	75.2	561	13	US-08-905-314-24
6	231.4	72.5	637	22	US-09-580-797-12
7	187	58.6	672	22	US-09-580-797-28
8	183.8	57.6	504	13	US-08-905-314-19
9	183.2	57.4	522	36	US-09-961-755A-5
10	183.2	57.4	522	36	US-09-961-755A-8
11	180.4	56.6	545	13	US-08-905-314-21
12	180	56.4	546	13	US-08-905-314-22
13	176.4	55.3	521	36	US-09-961-755A-6
14	174.8	54.8	503	13	US-08-905-314-20
15	171.4	53.7	504	18	US-09-481-293-32
16	167	52.4	620	22	US-09-580-797-11
17	156.8	49.2	611	1	PCT-US98-25210-4
18	145.6	45.6	608	1	PCT-US98-25210-3
19	134.2	42.1	382	16	US-09-241-427-3
20	128.4	40.3	605	1	PCT-US98-25210-1
21	126.6	39.7	365	18	US-09-423-233-3
22	125.8	39.4	617	1	PCT-US98-25210-2
23	123.2	38.6	365	18	US-09-423-233-5
24	122.6	38.4	599	22	US-09-580-797-37
25	121.2	38.0	364	18	US-09-423-233-2
26	118.6	37.2	608	22	US-09-580-797-38
27	118	37.0	568	1	PCT-US98-25210-5
28	117.8	36.9	7997	47	US-60-082-300-11599
29	117	36.7	727	22	US-09-580-797-29
30	116.2	36.4	597	22	US-09-580-797-35
31	115.8	36.3	551	52	US-60-132-861-9331


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Oy      2  aaatgcgataagtaatcttgaaattcgaaatccagtgaatactcgaactcttggaaagcac 61
Db      228  aaaatgcgataagtaatcttgaaattcgaaatccagtgaatactcgaactcttggaaagcac 287
Oy      62  atgcgcgcgcgcagatattctcgcgcgcgcacatgcctcttcagcgcgtcatltaacaacctcaagc 121
Db      288  attgccgcgcgcagatattctcgcgcgcgcacatgcctcttcagcgcgtcatltaacaacctcaagc 347
Oy      122  cccgcgcgcctcgcgtcttggggatcgcgcgcgaagccccctcgcgcgcacaaagccgtctcccccac 181
Db      348  cccgcgcgcctcgcgtcttggggatcgcgcgcgaagccccctcgcgcgcacaaagccgtctcccccac 400
Oy      182  atacgcgtgcgcgtccgcgcgcgcagccttccatctgcgtagtagtcaaacctcgcgaactggag 241
Db      401  atctagtcgcgcgtctcgcgcgtcgcgtctccatctgcgttagtagtaaaacctcgcgaacttgta 460
Oy      242  agcgcgcgcgcgcgcgcgcgcgttaaaacaccccaactctcgaatggttgacctcgtgaatcagttag 301
Db      461  cgcgcgcgcgcgcgcgcgcgcgttaaaacaccccaactctcgaatggttgacctcgtgaatcagttag 520
Oy      302  aataccgcctgaac 315
Db      521  aataccgcctgaac 534

RESULT 4
US-09-423-233-7
: Sequence 7, Application US/09423233
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America as
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 03063-0341MP
: CURRENT APPLICATION NUMBER: US/09/423,233
: CURRENT FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 310
: TYPE: DNA
: ORGANISM: Fusarium moniliforme
: US-09-423-233-7

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Query Match	75.3%	Score 240.2	DB 18	Length 310
Best Local Similarity	87.4%	Prod. No. 8.4e-61		
Matches 277	Conservative	0	Mismatches 33	Indels 7
				Gaps 1
QY	3 aatcgcataaataatgtcaattgcagaattcaagtcaatcaccgaattcttgaacgaca	62		
Db	1 aatcgcataaataatgtcaattgcagaattcaagtcaatcaccgaattcttgaacgaca	60		
QY	63 ttgcgcgccgcagatctctgcgcggcagtcgctgttcgagcgtcaatlaaacctcaagcc	122		
Db	61 ttgcgcgccgcagatctctctgcgcggcagtcgctgttcgagcgtcaatlaaacctcaagcc	120		
QY	123 cccgcggcctcgcggtttggggatctgcgcggaaagcccccctgcgcggcacaaagccgtcccccaca	182		
Db	121 cccgcgggtttcggtttggggatctgcgcgaagccctctgcgc-----aagccgcgcccgaga	173		
QY	183 tacagttgcgggtcccccgcagcttcacattctgttcgtaagtaacacctgcgaactcgaga	242		
Db	174 tctagtgcggtctcgccttcgctcagcttcacattctgttcgtaagtaaaacccctgcgaactcgatc	233		
QY	243 gcgcgcgcgcacgcgcgtlaaacaaccccaactctcgaattgttcgaactcgaaatcagtaga	302		
Db	234 gcgcgcgcgcacgcgcgtlaaacaaccccaactctcgaattgttcgaactcgaaatcagtaga	293		
QY	303 ataccgcctgaacttaa 319			
Db	294 ataccgcctgaacttaa 310			

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US-08-905-314-24
: Sequence 24, Application US/08905314
: GENERAL INFORMATION:
: APPLICANT: Beck, James J.
: TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Novartis Corporation Patent Department
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 20779-2257
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/905,314
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38, 241
: REFERENCE/DOCKET NUMBER: CGC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 561 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: STRAIN: Fusarium avenaceum
: INDIVIDUAL ISOLATE: 64452 and R-4045 (consensus sequence)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..30
: OTHER INFORMATION: /note= "3' end of small subunit"
: OTHER INFORMATION: rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 31..181
: OTHER INFORMATION: /note= "ITS 1"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 182..338
: OTHER INFORMATION: /note= "5.8S rRNA gene"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 339..504
: OTHER INFORMATION: /note= "ITS 2"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 505..561
: OTHER INFORMATION: /note= "5' end of large subunit"
: OTHER INFORMATION: rRNA gene"
US-08-905-314-24

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Best Local	88.7%	Pred. No. 1	1e-60		
Matches	282	Conservative	2	Mismatches	27
				Indels	7
				Gaps	2

Qy 2 aaaaatgcgaataagtaatgtaatgcagaatccatgtaatcgaatcgtgaacgcac 61

Db 231 AAAATCCGATTAAGTATTCGAATTCGATTCGAGATTCAGGATTCATTCGATTTTGAGCGCAC 290

[illegible]

RESULT 11
US-08-905-314-21
; Sequence 21, Application US/08905314

1 APPLICANT: Beck, James J.
 2 TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
 3 TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
 4 NUMBER OF SEQUENCES: 24
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: NOVARTIS Corporation Patent Department
 7 STREET: 3054 Cornwallis Road
 8 CITY: Research Triangle Park
 9 STATE: NC
 10 COUNTRY: USA
 11 ZIP: 20779-2257
 12 COMPUTER READABLE FORM:
 13 MEDIUM TYPE: Floppy disk
 14 COMPUTER: IBM PC compatible
 15 OPERATING SYSTEM: PC-DOS/MS-DOS
 16 SOFTWARE: PatentIn Release #1.0, Version #1.30
 17 CURRENT APPLICATION DATA:
 18 APPLICATION NUMBER: US/08/905,314

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: Mclg, J. Timothy
  REGISTRATION NUMBER: 38,241
  REFERENCE/DOCKET NUMBER: CCC 19444
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (919) 541-8587
  TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 21:
  LENGTH: 545 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
  ORGANISM: Fusarium moniliforme
  INDIVIDUAL ISOLATE: 4551
  IMMEDIATE SOURCE:
    CLONE: pCRMON1
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 1..30
  OTHER INFORMATION: /note="3' end"
  OTHER INFORMATION: rRNA gene"
FEATURE:
  NAME/KEY: misc_feature
  LOCATION: 31..178

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? OTHER INFORMATION: /note="ITS 1"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 179..335
? OTHER INFORMATION: /note="5.8S rRNA gene"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 336..488
? OTHER INFORMATION: /note="ITS 2"
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 489..545
? OTHER INFORMATION: /note="5' end of large subunit"
? OTHER INFORMATION: rRNA gene"
US-08-905-314-21

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Query Match	56.6%;	Score 180.4;	DB 13;	Length 545;
Best Local Similarity	82.4%;	Pred. NO. 6e-43;		
Matches 262;	Conservative 0;	Mismatches 36;	Indels 20;	Gaps 4;

QY	2	aaatcgataaagaaatgatgatggaattggaattggaatcaatgaattctttaaagccac	61
Db	228	AAATGCGCATAAATGTAATGTGATTTGCAAAATTCAGTAAATCATGGAATCTTTGAACCCAC	287
QY	62	atctgcgccgcagbaltcttgaggcgagatgcctgttctgaagcgtcatatacaacctcagc	121
Db	288	ATTCGCGCCCGCACATATCTTGCGCGGATGCGCTTGTGACGCTGATTTTCAACCTCAGC	347
QY	122	ccccggagcctgcgttggtagatcgagcggaagccccctgcggcgcaacagcgctcccca	181
Db	348	CC---AGCTTGCTTTGGGAGACTG-----CAGTCTGCTGCACCTCCCA	389
QY	182	atacagtagcgagtcgccgcgcgaagcttccattcgtagtagtaaacacttcgcacttagag	241
Db	390	ATACATTTGGCGGCTACACGTGC-AGCTTCCATAGCCTAGTAATTTACACATGTGTTACTGTGA	448
QY	242	agcgcgagcgacagcgcttlaaacaaccaacttctgaatttgaaccgcgaatagtagg	301
Db	449	ATTCGCGGGGCGACAGCGGTTAAAC-CCCACTTCTGAAATTTGACCTCGGATCAGTAGG	507
QY	302	ataccgcgcgtgaacttaa	319
Db	508	AATACCGGCTGAACCTTAA	525

RESULT 12
US-08-905-314-22
Sequence 22, Application US/08905314
GENERAL INFORMATION:
APPLICANT: Beck, James J.
TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novartis Corporation Patent Department
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 20779-2257
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,314
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241

```

REFERENCE/DOCKET NUMBER: CGC 1944
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Fusarium poae
INDIVIDUAL ISOLATE: T-427, T-534, and T-756 (consensus)
INDIVIDUAL ISOLATE: sequence)
IMMEDIATE SOURCE:
CLONE: pCRFpoaeT427(1-2), pCRFpoaeT534(2-2), and
CLONE: pCRFpoaeT756(3-1)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..30
OTHER INFORMATION: /note= "3' end of small subunit"
OTHER INFORMATION: rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 31..180
OTHER INFORMATION: /note= "ITS 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 181..337
OTHER INFORMATION: /note= "5.8S rRNA gene"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 338..489
OTHER INFORMATION: /note= "ITS 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 490..546
OTHER INFORMATION: /note= "5' end of large subunit"
OTHER INFORMATION: rRNA gene"
US-08-905-314-22

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	Query Match:	56.4%;	Score 180;	DB 13;	Length 546;	
	Best Local Similarity:	82.4%;	Pred. No. 7,9e-43;			
	Matches 262;	Conservative	0;	Mismatches 35;	Indels 21;	Gaps 4;
OY	2	aaaatcgataaagtgaattgcagaatcagatcgatgacatcgaactcttgaacgcaac	61			
Dd	230	AAAATGCGAATGAATATGTGATTTCAGAAATTCATGTAATCATCGAATCTTTGAACGCAC	289			
OY	62	atitgcgccgcagatattcttcggcggcatgtccctgttcgaagcgtcaatacacccctcaaggc	121			
Dd	290	ATTGGCGCCGCCAGTATTCGTGGCGGGCATGCTGTTGCAGCGATTTCAACCCTCMAAGC	349			
OY	122	cccccggcctgcgctttggggatcgcgcggaagccccttcgcgcgacaacgcgcgtcccccac	181			
Dd	350	CC--ACCTTGCGTGGTGG-----ATTGTGTGTCAAACACAGTCCCCCAA	390			
OY	182	ataacagtagcgatccscgcgcagcttcactctgcglagtagctaacaaccctgcgaactgag	241			
Dd	391	ATTGATTGGGGGTACAGTGC-AGCTTCCATTAGCGTAGTAATTTACACTGCTTACTGTGA	449			
OY	242	agcgcgcgcacgcgcgcgtlaaacaaccaccaactctcgaattgtltgacctgcgaatcagtag	301			
Dd	450	ATCTCGCCGGSCACAGCGCTTAAAC-CCCAACTTGTGAATGTGAACTCGGATCAGTAGG	508			
OY	302	aataccgcgtgaactaa	319			
Dd	509	AATAACCGCTGAACTTAA	526			

```

US-09-961-755A-6
: Sequence 6, Application US/09961755A
:
: GENERAL INFORMATION:
:
: APPLICANT: Beck, Jim
:
: APPLICANT: Barnett, Jason
:
: TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
:
: TITLE OF INVENTION: Polymerase Chain Reaction
:
: FILE REFERENCE: 60055
:
: CURRENT APPLICATION NUMBER: US/09/961,755A
:
: CURRENT FILING DATE: 2001-09-24
:
: NUMBER OF SEQ ID NOS: 24
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 6
:
: LENGTH: 521
:
: TYPE: DNA
:
: ORGANISM: Gibberella zeae
:
: US-09-961-755A-6

```

	Query Match	55.3%	Score 176.4	DB 36	Length 521	
	Best Local Similarity	82.2%	Pred. No. 9.2e-42			
	Matches 258	Conservative	0	Mismatches 36	Indels 20	Gaps 4
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Db	228 aaaatgcgataagtaatgtgaattcgacgaattcagaatctcaatgaacttcgaatccgac	287				
OY	62 attgcgccgcagcatattcttgcggcgacatgcctgtttcgacgtcatataaaccttcgac	121				
Db	288 attgcgccgcagcatattcttgcggcgacatgcctgtttcgacgtcatattacaaccttaaac	347				
OY	122 ccccgggcctgcgcttttgaggatcgcggaaagcccccttgcggcacaaagcgtlcccccaa	181				
Db	348 cc---agcttgttgtttggtagctg-----cagtcttcgcgcgaactccccaa	389				
OY	182 atacagatgcggtlcccgccgcagactccaattgcgtatgagcttaacacccttcgaactcgag	241				
Db	390 atacatitgcggtlcaacgtcg-agcttccctaagcgtatgaatttaaccatcgtlaactcyta	448				
OY	242 agcggcgcggccagcgcgtaaaacaccacaacttgaatgttgaactcgtgaatcagtagg	301				
Db	449 atcgttcgcggccagcgcgttaaacc-cccacacttctgaatgttgaactcgtgaatcagtagg	507				
OY	302 aatatccgcgtgaac	315				
Db	508 aataccgcgtgaac	521				

RESULT 14
 ; Sequence 20, Application US/08905314
 ; GENERAL INFORMATION:
 ; APPLICANT: Beck, James J.
 ; TITLE OF INVENTION: DETECTION OF WHEAT FUNGAL PATHOGENS
 ; TITLE OF INVENTION: USING THE POLYMERASE CHAIN REACTION
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Novartis Corporation Patent Department
 ; STREET: 3054 Cornwallis Road
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 20779-2257
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/905,314
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

```

: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CQC 1944
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 503 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Fusarium graminearum
: INDIVIDUAL ISOLATE: R-8417, R-8422, and R-8546
: INDIVIDUAL ISOLATE: (consensus sequence)
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1..9
: OTHER INFORMATION: /note="3' end of small subunit"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 10..155
: OTHER INFORMATION: /note="ITS 1"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 156..312
: OTHER INFORMATION: /note="5.8S rRNA gene"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 313..466
: OTHER INFORMATION: /note="ITS 2"
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 467..503
: OTHER INFORMATION: /note="5' end of large subunit"
:
: OTHER INFORMATION: rRNA gene"
:
: US-08-905-314-20

```

```

Query Match          54.8%; Score 174.8; DB 13; Length 503;
Best Local Similarity 78.0%; Pred. No. 2.7e-41;
Matches 248; Conservative 14; Mismatches 37; Indels 19; Gaps 4;

QY 2 aaaaatgcgaataatgtaattgtaattgcagaattcagtgaaatcagaatccttgaagcac 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 205 AAATGCGATAAATAATGTMATTCAGAAATTCAGTCAATCAACGAATCTTGAACGCS 264

QY 62 atgcgcgcgcagatctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 265 ATTGCKMKCCRCAGTATTCTGGCGGCATGCCGTTCGAGCGCATTTCAACCCCTCAAGC 324

QY 122 ccccgagccctgcgttgaggatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 181
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 325 CC---AGVTTGGTGTGKGGAARYTC-----AGKCTRYTKCACTCCCA 367

QY 182 atacaatgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 241
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 368 ATTAATTGGCGGTCACCTGC-AACTTCATAGCGTAACTAGTACATCGTTACTGTA 426

QY 242 agcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 301
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 427 ATCGTGGCGGCTACGCCGTAAAC-CCCAACTCTGAATGTTGACCTCGATCAGGTAG 485

QY 302 aataccgcctgaactaa 319
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 486 AATACCCGCTGAAGTAA 503

```

RESULT 15
US-09-481-293-32

```

: Sequence 32, Application US/09481293
: GENERAL INFORMATION:
: APPLICANT: Beck, James
: TITLE OF INVENTION: PCR-Based Detection of Rhizoctonia cerealis
: FILE REFERENCE: PB/5-31135p1
: CURRENT APPLICATION NUMBER: US/09/481,293
: CURRENT FILING DATE: 2000-01-11
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 32
: LENGTH: 504
: TYPE: DNA
: ORGANISM: Fusarium culmorum
:
: US-09-481-293-32

```

```

Query Match          53.7%; Score 171.4; DB 18; Length 504;
Best Local Similarity 81.4%; Pred. No. 2.8e-40;
Matches 253; Conservative 1; Mismatches 37; Indels 20; Gaps 4;

QY 2 aaaaatgcgaataatgtaattgtaattgcagaattcagtgaaatcagaatccttgaagcac 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 214 aaaaatgcgaataatgtaattgtaattgcagaattcagtgaaatcagaatccttgaagcac 273

QY 62 atgcgcgcgcagatctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 274 atgcgcgcgcagatctctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 333

QY 122 ccccgagccctgcgttgaggatctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 181
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 334 CC---agcttggtgtggagactg-----cagtcctctgcagcaccacca 375

QY 182 atacaatgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 241
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 376 atacaatgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 434

QY 242 agcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 301
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 435 atgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 493

QY 302 aataccgcctg 312
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 494 aataccgcctg 504

```

Search completed: August 22, 2002, 00:39:28
Job time: 13053 sec

[illegible]

Accession	Sequence	Position
D8	161 aatacagtcggtccgcgcgaagcttccattgctgaagtaaacactctgcacacttga	240
Qy	241 gagcgcgcgcgcgcacacgcgtlaaaacacccaaactcttgatgttgcacctgcgaatcagttag	300
D8	241 gagcgcgcgcgcgcacacgcgtlaaaacacccaaactcttgatgttgcacctgcgaatcagttag	300
Qy	301 gaataccgcgtgaactaa	319
D8	301 gaataccgcgtgaactaa	319

```

RESULT 2
US-10-046-955-7
: Sequence 7, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Etrol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046, 955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 7
: LENGTH: 310
: TYPE: DNA
: ORGANISM: Fusarium moniliforme
US-10-046-955-7

```

Query Match	75.3%	Score 240.2	DB 7	Length 310
Best Local Similarity	87.48%	Pred. No. 7.9e-61		
Matches 277; Conservative	0	Mismatches 33	Indels 7	Gaps 1

OY	3	aaatgcatgaatgaatgtgaattgaaagattcaatgaaatctcgaaatcttggaaacgaca	62
Db	1	aaatgcatgaatgaatgtgaattgaaatctgaataaatactgaatcaatcttggaaacgaca	60
OY	63	ttgcgcacccgcacgaatcttcgcgcgcgcacatgcttgcgcgcgtcatacaaaccttcagcc	122
Db	61	ttgcgcacccgcacgaatcttcgcgcgcgcacatgcttgcgcgcgtcataatccaacctcaagcc	120
OY	123	ccgcgcgccttgccgtttggggatcgcgcgcgaagaccccttcgcgcgcacaaagccgctcccccaaa	182
Db	121	ccgcgcgccttcgtgtgttggggatcgcgcgcgaagcccttcgcgcgc-----aaagccgcgcctccgcaaaa	173
OY	183	tacagttgcgcgcgttccgcgcgcacgcttccatctgcgtgagtagctaaacacttcgcgaactgtgaga	242
Db	174	tctagtcgcgcgtcttcgcgcgcagcttccatctgcgtgagtagtaaaaccttcgcaactgtctac	233
OY	243	gcgcgcgcgcgcacgcgcgcgaaaaaaccccaacttcgaatgtttgaaccttgaaatcaggtagga	302
Db	234	gcgcgcgcgcgcacgcgcgcgtctataaaccccaacttcgaatgttgaaacttcgatacaggtagga	293
OY	303	ataccgcgtgaacttaa	319
Db	294	ataccgcgtgaacttaa	310

RESULT 3

```

PCT-US02-11769-2
: Sequence 2, Application PC/TUS0211769
: GENERAL INFORMATION:
: APPLICANT: Strobel, Gary
: APPLICANT: Manker, Denise
: TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
: TITLE OF INVENTION: USE
: FILE REFERENCE: AQ 2019_40
: CURRENT APPLICATION NUMBER: PCT/US02/11769
: CURRENT FILING DATE: 2002-04-11
: PRIOR APPLICATION NUMBER: 60/283,902
: PRIOR FILING DATE: 2002-03-11
: PRIOR APPLICATION NUMBER: 60/363,072
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ. ID NOS.: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 2
: LENGTH: 652
: TYPE: DNA
: ORGANISM: Muscador albus
PCT-US02-11769-2

```

Query Match	41.3%	Score 131.8;	DB 1;	Length 652;
Best Local Similarity	72.6%;	Pred. No. 5.8e-29;		
Matches 230; Conservative	0;	Mismatches 72;	Indels 15;	Gaps 4

QY	3	aaatgagcaataagtaatggaattgcagaattcagtgaaatcaatcgaattctttgaacgcaca	62
Db	329	aaagacgcaataagaaagtgaaattgcagaattcagtgaaatcatatgaattctttgaacgcaca <td>386</td>	386
QY	63	tgcgcgcgcgcagcaattcttcgcgcgcacatgcctgttctgaagcgtcatatcaaaccttcagacc	122
Db	389	tgcgcgcattagcatcttcagtgaggacgtctgttcgagcgtcatatcgaacttcaacctaagacc	446
QY	123	cgcgcgcgcgcgttgaggagatcgcgcgaagcccccctgcgcgcacaaacgcgttcccccaa	187
Db	449	ctgttgcctaaagcttgcggagacctacgcgaactgc-----cgtlaagctccctaa	496
QY	183	tacagtcgcgcgtgccgcgcgcagacttcatttcgctgaatgaatcaaaccttcgcacgtgcaga	242
Db	497	gttatgtgcgcgcaggttcgtttcactctta-ggcgtgaatatt-ctatctgcctctgtgaat	554
QY	243	gcgcgcgcgcgcacgcgcgtgaanaaacccaacttcgaatttgactgcgaatcagtagga	302
Db	555	ggttcgcgcgcctcgcgcgaanaaacccccaatc-aaaggttgacctgcgaatcagtagga	613
QY	303	ataccgcctgaacttaa	319
Db	614	ataccgcctgaacttaa	630

RESULT 4
US-10-046-955-3
Sequence 3, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reiss, Etrol
APPLICANT: Aldorevich, Lilliana
APPLICANT: Choi, Jong Soo
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE OF INVENTION: Other Filamentous Fungi
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400

```

; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-046-955-3

```

Query Match	39.7%	Score 126.6;	DB 7;	Length 365;
Best Local Similarity	64.7%	Pred. No. 1.7e-27;		
Matches 205; Conservative	0;	Mismatches 109;	Indels 3;	Gaps 1;

[illegible]

```

RESULT      5
US-10-046-955-5
: Sequence 5, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Disease Control and Prevention
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lilliana
: APPLICANT: Chol, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046, 955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423, 233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 5
: LENGTH: 365
: TYPE: DNA
: ORGANISM: Aspergillus nidulans
US-10-046-955-5

```

Query Match	38.68;	Score 123.2;	DB 7;	Length 365;
Best Local Similarity	66.08;	Pred. No. 1.7e-26;		
Matches 210; Conservative	0;	Mismatches 103;	Indels 5;	Gaps 2

[illegible]

```

: RESULT 6
: US-10-046-955-2
: Sequence 2, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lilliana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: FILE REFERENCE: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046, 955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423, 233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045, 400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 364
: TYPE: DNA
: ORGANISM: Aspergillus fumigatus
: US-10-046-955-2

```

	Query Match	38.0%;	Score 121.2;	DB 7;	Length 364;
	Best Local Similarity	65.9%;	Pred. No. 6.7e-26;		
	Matches 211;	Conservative	0;	Mismatches 98;	Indels 11; Gaps 2;
OY	3 aaatgcgataagtaattgaaattgcagaattgaagatcatcgaattctttaaagccaca	62			
DB	52 aaatgcgataactaatgtbaatttcgaagaattcaatgaacatcgattctttaacygaca	111			
OY	63 ttggcccccgcgcgatatttcygcgagcatgccgttttcgaagcgfcatcaaacaccttaagcc	122			
DB	112 ttgcgcccccttgatttcgcgggggacagcctgttcgcagcgfcatlctgcgccatcaagc	171			
OY	123 ccgcggcctgtgcgtttgggagtgcgcggaagcccccttcyggcacacaacgcgcgtcccca	182			
DB	172 acgagcttgttatltttgcgccccctatcccccttccgcagg-----aacgggaccgaaa	223			


```

; Sequence 26, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
; APPLICANT: Control and Prevention
; APPLICANT: Morison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Scedosporium apiospermum
; US-10-046-955-26

Query Match          34.5%; Score 110.2; DB 7; Length 344;
Best Local Similarity 68.7%; Pred. No. 1.1e-22;
Matches 237; Conservative 0; Mismatches 78; Indels 30; Gaps 5;

OY 3 aatgcgataagaatgtaattgcagaattcagtaacatcgaattcttgaacgcaca 62
    |||||||
DB 2 aatgcgataagaatgtaattgcagaattcagtaacatcgaattcttgaacgcaca 61
    |||||||

OY 63 ttgcgcgcgcagatctctgcgcgagcagctgttcgagcgatcacaacccctcaggcc 122
    |||||||
DB 62 ttgcgcgcgcagatctctgcgcgagcagctgttcgagcgatcacaacccctcaggcc 121
    |||||||

OY 123 cccg-----ggcctggtgttggtggtatcgcggaagccccccttgcgggca 165
    |||
DB 122 tccgcttctcctcaggaagctcagggctcggtcttggtggcgctcagcgagctctcgagcc 181
    |||

OY 166 caagcgctccccaataacagctgagcgtcccgccgagctccat-tgcgtagtagccta 224
    |||
DB 182 ctccgtaagccctgaataacagctgagcgtcccgccgagctctccttgcgtagtagccta 241
    |||

OY 225 aaaccctgcga-----actggagagcgcgcgccacgctgaacaaacccaacttcgta 278
    |||
DB 242 tctttgcagaatcgatcggtggtcccggtcggtggtggtccttcgcaaacccaactatactcc 301
    |||

OY 279 a-----tgtgacctcgatcagtaggaatacccgctgaactaa 319
    |||||||
DB 302 agatggttgacctcgatcagtaggaatacccgctgaactaa 344
    |||||||

RESULT 13
; Sequence 5, Application US/09517790
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F
; TITLE OF INVENTION: Use of Ploma glomerata as a Hyperparasite in the Biocontrol of Fy
; FILE REFERENCE: RU-0093
; CURRENT APPLICATION NUMBER: US/09/517,790
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/123,099
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5

```

```

; LENGTH: 536
; TYPE: DNA
; ORGANISM: Ampelomyces humu11
; US-09-517-790-5

Query Match          34.3%; Score 109.4; DB 5; Length 536;
Best Local Similarity 66.2%; Pred. No. 2.1e-22;
Matches 210; Conservative 0; Mismatches 91; Indels 16; Gaps 3;

OY 3 aatgcgataagaatgtaattgcagaattcagtaacatcgaattcttgaacgcaca 62
    |||||||
DB 220 aatgcgataagaatgtaattgcagaattcagtaacatcgaattcttgaacgcaca 279
    |||||||

OY 63 ttgcgcgcgcagatctctgcgcgagcagctgttcgagcgctcacaacccctcaggcc 122
    |||||||
DB 280 ttgcgcgcgcagatctctgcgcgagcagctgttcgagcgctcacaacccctcaggcc 337
    |||||||

OY 123 cccgagcctggtgttggtggtatcgcggaagcccccctcgcggaacagcgctcccaaa 182
    |||
DB 338 -----ctcgcttggtgttggtgttcttcgctctcggtgtagtactcgctcctcaaa 390
    |||

OY 183 tacagtgcggttcccgccagctccatctgctgtagtagtaacacactcggaactggaga 242
    |||
DB 391 acaattgg-----cagccggtgattgattcggagcgagtagatctcggtcttcac 445
    |||

OY 243 ggcgcgcgcgcagcgcgtaaacacccaactctgaatgttgacctcgaaatcagtagga 302
    |||
DB 446 tcaatcagcagcagctcccaagta--cattttacactctgacctgagatcagtaggag 503
    |||

OY 303 ataccgctgaactaa 319
    |||||||
DB 504 ataccgctgaactaa 520
    |||||||

RESULT 14
; Sequence 25, Application US/10046955
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary of the Department of Health and Human Services, Centers for
; APPLICANT: Control and Prevention
; APPLICANT: Morison, Christine J.
; APPLICANT: Reiss, Errol
; APPLICANT: Aldorevich, Lilliana
; APPLICANT: Choi, Jong Soo
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT APPLICATION NUMBER: US/10/046,955
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Pseudallescheria boydii
; US-10-046-955-25

Query Match          34.2%; Score 109.2; DB 7; Length 346;
Best Local Similarity 70.2%; Pred. No. 2.2e-22;
Matches 243; Conservative 0; Mismatches 73; Indels 30; Gaps 6;

OY 3 aatgcgataagaatgtaattgcagaattcagtaacatcgaattcttgaacgcac 61
    |||||||
DB 2 aatgcgataagaatgtaattgcagaattcagtaacatcgaattcttgaacgcac 61
    |||||||

```

[illegible]

```

RESULT 15
US-10-046-955-28
: Sequence 28, Application US/10046955
: GENERAL INFORMATION:
: APPLICANT: The Government of the United States of America, as Represented by the
: APPLICANT: Secretary of the Department of Health and Human Services, Centers for Dis
: APPLICANT: Control and Prevention
: APPLICANT: Morrison, Christine J.
: APPLICANT: Reiss, Errol
: APPLICANT: Aldorevich, Lillana
: APPLICANT: Choi, Jong Soo
: TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
: TITLE OF INVENTION: Other Filamentous Fungi
: FILE REFERENCE: 6395-62064
: CURRENT APPLICATION NUMBER: US/10/046,955
: CURRENT FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US 09/423,233
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: PCT/US98/08926
: PRIOR FILING DATE: 1998-05-01
: PRIOR APPLICATION NUMBER: US 60/045,400
: PRIOR FILING DATE: 1997-05-02
: NUMBER OF SEQ ID NOS: 61
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 28
: LENGTH: 309
: TYPE: DNA
: ORGANISM: Penicillium notatum
US-10-046-955-28

```

Query Match	33.98;	Score 108;	DB 7;	Length 309;
Best Local Similarity	67.58;	Pred. No. 4.9e-22;		
Matches 216; Conservative	0;	Mismatches 90;	Indels 14;	Gaps 4

[illegible][illegible]

Search completed: August 22, 2002, 00:50:49
Job time: 11889 sec

|

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:47 ; Search time 2238.68 Seconds
(without alignments)
2897.791 Million cell updates/sec

Title: US-10-046-955-7

Perfect score: 1 aaatgcataagcaatgta.....ggataccgcgtgaacttaa 310

Sequence: 1 aaatgcataagcaatgta.....ggataccgcgtgaacttaa 310

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hhg_hum:*
31: em_hhg_inv:*
32: em_hhg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	310	100.0	310	8	AF117922	AF117922	Gibberella
2	306.8	99.0	351	8	AF162903	AF162903	Fusarium
3	306.8	99.0	558	8	FEUJRNA	X94176	Fusarium fu
4	306.8	99.0	558	8	FPORRNA	X94171	Fusarium pr
5	306.8	99.0	569	8	AF452163	AF452163	Pythium u
6	306.8	99.0	596	8	AF291061	AF291061	Fusarium
7	306.8	99.0	2293	6	ARI68094	ARI68094	Sequence
8	305.2	98.5	531	8	AF158303	AF158303	Fusarium
9	305.2	98.5	540	8	AF158304	AF158304	Fusarium
10	303.6	97.9	540	8	AF158302	AF158302	Fusarium
11	302.8	97.7	534	8	FEU34557	FEU34557	Fusarium fu
12	302.8	97.7	534	8	FEU34558	FEU34558	Fusarium pr
13	301.2	97.2	534	8	FAU61670	FAU61670	Fusarium an
14	301.2	97.2	534	8	FSU61693	FSU61693	Fusarium sp
15	300.8	97.0	502	8	AF165873	AF165873	Gibberella
16	299.6	96.6	534	8	FPURRNA	X94177	Fusarium ph
17	297.2	95.9	559	8	FREDRNA	X94169	Fusarium re
18	296.4	95.6	534	8	FSU34567	FSU34567	Fusarium sp
19	296.4	95.6	534	8	FSU61692	FSU61692	Fusarium sp
20	294.8	95.1	534	8	FSU34564	FSU34564	Fusarium sp
21	294.2	94.9	541	8	AF158307	AF158307	Fusarium
22	294.2	94.9	541	8	AF158309	AF158309	Fusarium
23	294.2	94.9	559	8	FDLARNNA	X94177	Fusarium dl
24	291	93.9	527	8	FSU61687	FSU61687	Fusarium q1
25	290.8	93.8	521	8	FSU61691	FSU61691	Fusarium ap
26	290.2	93.6	535	8	FAU34573	FAU34573	Fusarium ac
27	290	93.5	535	8	FSU34565	FSU34565	Fusarium re
28	289.2	93.3	522	8	FCU61678	FCU61678	Fusarium co
29	289	93.2	542	8	AF008920	AF008920	Fusarium
30	288.6	93.1	535	8	FDU34572	FDU34572	Fusarium dl
31	288.4	93.0	349	8	AF162897	AF162897	Fusarium
32	288.4	93.0	529	8	AF158312	AF158312	Fusarium
33	288.4	93.0	557	8	FNCRRNA	X94174	Fusarium ny
34	284.4	91.7	533	8	FN034568	FN034568	Fusarium ny
35	284.4	91.7	533	8	FU034575	FU034575	Fusarium ud
36	278.2	89.7	543	8	FBU34581	FBU34581	Fusarium bu
37	272.4	87.9	532	8	FSU34560	FSU34560	Fusarium th
38	270.8	87.4	520	8	FSU61690	FSU61690	Fusarium th
39	270.8	87.4	1458	8	AF310981	AF310981	Fusarium ap
40	269.2	86.8	538	8	PPU18954	PPU18954	Pseudofusar
41	268.4	86.6	538	8	FSU61695	FSU61695	Fusarium sp
42	267.2	86.2	471	8	AF150468	AF150468	Nectria h
43	267.2	86.2	1460	8	AF310976	AF310976	Fusarium
44	267.2	86.2	1460	8	AF310977	AF310977	Fusarium
45	266.8	86.1	1456	8	AF310982	AF310982	Fusarium

ALIGNMENTS

RESULT 1
AF117922
LOCUS 310 bp DNA linear PLN 17-JUN-2000
DEFINITION Gibberella fujikuroi ATCC 38519 5.8S ribosomal RNA gene, partial
sequence; Internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
ACCESSION AF117922
VERSION AF117922.1 GI:8570108
KEYWORDS
SOURCE
ORGANISM

Gibberella fujikuroi.
Gibberella fujikuroi
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
REFERENCE
1 (bases 1 to 310)
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Rapid differentiation of filamentous fungi using species-specific
DNA probes
JOURNAL Abstr. Gen. Meet. Am. Soc. Microbiol. 98, C288 (1998)
REFERENCE
2 (bases 1 to 310)
Choi, J.S., Westerman, J.M. and Morrison, C.J.
Direct Submission
Submitted (09-SEP-1998) DBMD, CDC, 1600 Clifton Rd., Atlanta, GA
30333, USA

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FEATURES
    source
        location/Qualifiers
            1..310
                /organism="Gibberella fujikuroi"
                /strain="ATCC 38519"
                /db_xref="ATCC:38519"
                /db_xref="taxon:5127"
            <1..159
                /product="5.8S ribosomal RNA"
            159..272
                /note="ITS2"
            /product="internal transcribed spacer 2"
            273..>310
                /product="28S ribosomal RNA"
    BASE COUNT
        73 a      86 c      80 g      71 t
    ORIGIN

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	Query Match:	Score 310;	DB 8;	Length 310;	100.0%;
	Best Local Similarity	100.0%;	Pred. No. 4,6e-85;		
	Matches 310;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	aalgcgataagtaatcgtgaattcgcaaaatctcagtgaaatcatcgaatcctttgaacgaca	60		
Db	1	AATGCCGATAGTAATGTGAATTGCAAAATTCAGTAAATCATCCAACTTTGGAACCCACA	60		
Oy	61	ttagccgccgcaatatcttcggcgacatgcctgttccgagcgctaattccaacctcaagcc	120		
Db	61	TTGGCCCCCGCACTATTCTGGCGGCGATGCTGTTCGAGCGTCATTTCACCTCAGACC	120		
Oy	121	cccgggttttggttggttgaggatcgcgaagaccctltcgagaaacgcgcgcgaagaactagtg	180		
Db	121	CCCGGTTTTGCTGTTGGGATGCGCAACCCCTTGCGGCAACCGCCGCCAATAATCTAGTG	180		
Oy	181	ggaggttcgtcgtgagatlcgatctgtgtagtgtgttaaaccctcgaacttgttaacgggc	240		
Db	181	GGCGTCTCGCTGACGCTTCATTCGCTGTAAGTAAACCTTCGCACTGGTAGCGGCGC	240		
Oy	241	ggccaaagccgttaaaccccccaactctgaatgtttgacctcggatcaggtagaataccg	300		
Db	241	GGCCAAAGCGGTTAAACCCCACACTCTGAATGTGACCTCGATCAGGTAGGAATACCG	300		
Oy	301	cigaacttaa	310		
Db	301	CTGACTTAA	310		
RESULT 2					
LOCUS	AF162903	351 bp	DNA	linear	PLN 04-AUG-1999
DEFINITION	Fusarium proliferatum 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.				
ACCESSION	AF162903				
VERSION	AF162903.1	GI:5690392			
SOURCE	Fusarium proliferatum.				
ORGANISM	Fusarium proliferatum. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex Min,B.R.				
REFERENCE	1 (bases 1 to 351)				
AUTHORS	Direct Submission				
JOURNAL	Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea				
FEATURES	Location/Qualifiers				
source	1..351				
	/organism="Fusarium proliferatum"				
	/strain="6787"				
	/db_xref="taxon:42674"				
rRNA	<1..128				
	/product="5.8S ribosomal RNA"				
misc_RNA	129..293				
	/product="internal transcribed spacer 2"				

	IRNA	294..>351	/product="28S ribosomal RNA"	
BASE COUNT	87 a	94 c	94 g	76 t
ORIGIN				
Query Match		99.0%; Score 306.8;	DB: 8;	Length 351;
Best Local Similarity		99.4%; Pred. No. 4,6e-84;		
Matches 308;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Db	1	aatgcgataaglaatgatgaattgcacaaatlccagtgaaatcagatcatcgatcctttgaagcaaca	60	
OY	22	AAATGCCCATAGTAAGTGAATTGCAGATTACGATTCATCCAAACTTTGAACCACACA	81	
Db	61	ttagccccgcacatcttcgcggcgacatgccttgcgttcgcaggctcaattccaaccttaagcc	120	
OY	82	TTCGGCCCCGCGCAATATCTTGCGCGGCGATCCTGTTCGAGCGCTCAATTCCAACCCCTCAAGCC	141	
Db	121	cccgggttggtgttggtggatcgcgaacgcccttgcgcgaacgcggcccgcgaatatagtgtg	180	
OY	142	CCCGGGTTTTGGTGTGGGATCGCGACCCCTTGGCGCAACCGCGCCCGCAAATCTAAGTG	201	
Db	181	ggcggctcgcgtgagcttcattcttgtgtgtgtgttaaaccctcgaaattgtttaaggcgcc	240	
OY	202	GCGGTCTCGCTGCGAGCTTCCATTGGGTGATGTATAAACCCCTCGGAACGTGATGCGGCGCG	261	
Db	241	ggccaaagccgtltaaaccccccaactctctaagtltgacctcgatcacagtlagaatalaccg	300	
OY	262	GGCCAAAGCCCTTAACCCCACTCTGTAATGTGACCTCGATCGAGTAGTAATACCG	321	
Db	301	ctgaacttaa	310	
OY	322	CTGAACTTAA	331	

	RESULT	3
FFUURRNA		
LOCUS	558 bp	DNA linear PLN 14-JUN-2001
DEFINITION	Fusarium fujikuroi 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2).	
ACCESSION	X94176	X93900
VERSION	X94176.1	GI:1122868
KEYWORDS	18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; Internal transcribed spacer 1; Internal transcribed spacer 2; ITS1; ITS2.	
SOURCE	Gibberella fujikuroi.	
ORGANISM	Gibberella fujikuroi Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex 1 (bases 1 to 558)	
REFERENCE	Maalwijk,C., de Koning,J.R.A., Baayen,R.P. and Gams,M. Discordant groupings of Fusarium spp. from sections Elegans, liseola and Diamantina a based on ribosomal ITS1 and ITS2 sequences Mycologia 88, 361-368 (1996)	
AUTHORS	2 (bases 1 to 558) Maalwijk.C.	
TITLE	Direct Submission	
JOURNAL	Submitted (08-DEC-1995)	
REFERENCE	C. Maalwijk, Research Inst. for Plant Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS	
JOURNAL	On Jun 15, 2001 this sequence version replaced gi:1103564.	
COMMENT	Overlaps with X78260.	
FEATURES	Location/Qualifiers	
source	1..558	
	/organism="Gibberella fujikuroi"	
	/strain="CBS 221.76"	
	/specific_host="rice"	
	/db_xref="taxon:5127"	
rRNA	<1..30	
	/gene="18S rRNA"	
	/product="18S ribosomal RNA"	
gene	1..30	
	/gene="18S rRNA"	

	misc-feature	31..177	/note="internal transcribed spacer 1, ITS1"
	rRNA	178..335	/gene="5.8 rRNA" /product="5.8 ribosomal RNA"
	gene	178..335	/gene="5.8 rRNA"
	misc-feature	336..500	/note="internal transcribed spacer 2, ITS2"
	rRNA	501..>558	/gene="28S rRNA"
	gene	501..558	/product="28S ribosomal RNA"
		/gene="28S rRNA"	
BASE COUNT	144 a	152 c	137 g
ORIGIN			125 t
Query Match	99.0%	Score 306.8:	DB 8: Length 558:
Best Local Similarity	99.4%	Pred. NO. 4.9e-84:	
Matches	308: Conservative	0: Mismatches	2: Indels
			Gaps 0:
OY	1	aatcgataagtaattgaattgcgcaaaatgaatcgaatcatcgaattcttgaaccaca	60
Db	229	AATATCGATAAGTAATTGATTTGCAGATTGATGAATCATCGAATCTTGTAAAGCCACA	288
OY	61	tltcgccgccgcaglatlcttcgcgggacalgccttcgttcgaagcgatcattcaacctcaagcc	120
Db	289	TTCGCCGCCGCCAGTATTTCTGGCGGGCAGTCCGTTTGACCGTCATTTCACCCCTCAAGCC	348
OY	121	cgcggglltgttgtttgaggatcgcgaagcccttcgcgcaagccgcggcccgaactagt	180
Db	349	CCCCGGTTTGGCTGTTCGGCATCGCCGAGCCCTTCGCGCMAAGCCGCCCGGAATCTAGTC	408
OY	181	gcggatcgcgcgcaccticcatcttcgatgtagaataaaccttcgcaactgtagtacggggcgc	240
Db	409	GGGGTCTCGCTCACCTTCATTGGGTATTAATAAACCTTCGAACCTGTACGGCGGCC	468
OY	241	ggccaagccggtlaaaccccccaactctcgaatgttcgaccccgatcagtaggaataccgcg	300
Db	469	GGCCAAGCCGTTAAACCCTTCGACTTCTGATTTGTACCTCGGATCAGTAGAATACCGC	528
OY	301	ctggaacttaa	310
Db	529	CTGAAGCTTAA	538
RESULT	4		
FPFORRNA			
LOCUS	FPFORRNA	558 bp	DNA linear PLN 14-JUN-2001
DEFINITION	Fusarium proliferatum 18S rRNA gene (partial), 5.8S rRNA gene, 28S		
KEYWORDS	rRNA gene (partial). internal transcribed spacer 1 (ITS1) and		
INTERNAL TRANSCRIBED SPACER 2 (ITS2).	X94171.X93904		
ACCESSION	X94171.1	GI:1122873	
VERSION	18S ribosomal RNA; 18S rRNA gene; 28S ribosomal RNA; 28S rRNA gene;		
KEYWORDS	5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1;		
INTERNAL TRANSCRIBED SPACER 2; ITS1; ITS2.	Fusarium proliferatum.		
SOURCE	Fusarium proliferatum.		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
REFERENCE	Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.		
AUTHORS	1 (bases 1 to 558)		
TITLE	Maaliwijk, C., de Koning, J.R.A., Baayen, R.P. and Gams, W.		
JOURNAL	Discordant groupings of Fusarium spp. from sections Elegans,		
REFERENCE	Liseola and Diamantina a based on ribosomal ITS1 and ITS2 sequences		
AUTHORS	Mycologia 88, 361-368 (1996)		
TITLE	2 (bases 1 to 558)		
JOURNAL	Maaliwijk, C.		
REFERENCE	Direct Submision		
AUTHORS	Submitted (08-DEC-1995) C. Maaliwijk, Research Inst. for Plant		
TITLE	Protection, PO box 9060, 6700 GW Wageningen, NETHERLANDS		
COMMENT	On Jun 15, 2001 this sequence version replaced gi:1103572.		

FEATURES	Overlaps with X/8260.	Location/Qualifiers
source	1..558	/organism="Fusarium proliferatum" /strain="CBS 217.76" /specific_host="Cattleya" /db_xref="taxon:42674"
rRNA	<1..30	/gene="18S rRNA" /product="18S ribosomal RNA"
gene	1..30	/gene="18S rRNA"
misc_feature	31..177	/note="Internal transcribed spacer 1, ITS1"
rRNA	178..335	/gene="5.8 rRNA"
gene	178..335	/product="5.8 ribosomal RNA"
misc_feature	336..500	/gene="5.8 rRNA"
rRNA	501..558	/note="Internal transcribed spacer 2, ITS2"
gene	501..558	/gene="28S rRNA"
gene	501..558	/product="28S ribosomal RNA"
BASE COUNT	144 a 152 c 137 g 125 t	
ORIGIN		
Query Match	99.0%; Score 306.8; DB 8; Length 558;	
Best Local Similarity	99.4%; Pred. No. 4.9e-84;	
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY 1	aaatcgataagtaattgtgaattgcacaaatcagtgatcagatcagatcttgaacgcaca 60	
Db 229	AAATCGATAAATGTAATGTGAATTCAGAAATTCAGAAATCATCGAATCTTTGAAACGACACA 288	
QY 61	tttgcgccccgcagattcttcgcgggcgatgcctgttcgagcgatcattcgaacctgaagc 120	
Db 289	TTGGCCCGCCCGACGATTTCTGCGGGCATGCTCTTCGACGATCTTCAACCTTAAGCC 348	
QY 121	cccgagtttgatgttgggagatcgcgaagcccttcgcgaagcgcgccccgaatatagtg 180	
Db 349	CCCGGTTTGGGTGTGGGATGCGGAGCCCTTTCGCGAAGCCGCCCGGAATCTAGTG 408	
QY 181	ggagctcgtgcgtcgaactccatctgtgtagttaaaacctgcgaactggtacggcgcg 240	
Db 409	GCGGCTCGCTCAGCTTCATTCATTTGGTAGTAATAAACCTTCGCAACTGTGACGGGCGC 468	
QY 241	ggcgaagcgtttaaaccgcccaactctgaattgtgaactcgtgatcagtgatgaataccgg 300	
Db 469	GGCCAAGCGGTAAACCCCAACTCTGATAGTTGACCTCGGATCAGGTAGGAATACCCG 528	
QY 301	ctgaacttaa 310	
Db 529	CTGAACCTTAA 538	
RESULT 5		
AF452163	AF452163	569 bp DNA linear PLN 27-DEC-2001
LOCUS	Pythium ultimum var. sporangififerum isolate 308276R 18S ribosomal	
DEFINITION	RNA gene, partial sequence.	
ACCESSION	AF452163	
VERSION	AF452163.1 GI:17980882	
KEYWORDS		
SOURCE	Pythium ultimum var. sporangififerum.	
ORGANISM	Pythium ultimum var. sporangififerum	
REFERENCE	1 (bases 1 to 569)	
AUTHORS	Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.	

TITLE Pythium species and a population identification using DNA markers
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 569)
AUTHORS Moorman,G.W., Geiser,D.M., Kang,S. and Kim,S.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2001) Plant Pathology, Pennsylvania State University, 210 Buckhout Laboratory, University Park, PA 16802, USA
LOCATION/Qualifiers
source 1..569
/organism="Pythium ultimum var. sporangiferum"
/variety="sporangiferum"
/isolate="308276R"
/db_xref="taxon:115421"
<1..569
/product="18S ribosomal RNA"
BASE COUNT 149 a 155 c 137 g 128 t
ORIGIN

Query Match 99.0% Score 306.8; DB 8; Length 569;
Best Local Similarity 99.4%; Pred. No. 4.9e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aatgagtaagtaatggaatgcaaatcagtaataatcgaatcttgaacgcaca 60
|||||
DB 246 AATGCGATGAATGTAATGCAATTCAGATTCACTGATCATCGAATCTTGAACGCACA 305
|||||
OY 61 ttgcgccgcagatattctgcgagcgatgcctgttcgagcgcaattcaaccctcaagcc 120
|||||
DB 306 TTGCGCCGCCAGTATTCGTGGCGGCAATGCCTGTTCGAGCGCTCATTTCAACCCCAAGCC 365
|||||
OY 121 cccgggttggtgttgaggatcggaacgacctgtgcgcaagcgcgcccgaaatcagtgtg 180
|||||
DB 366 CCCGGGTTGGTGTGGGGATCGCGAGCCCTTGCAGCAGCCGCCCGCAAACTCTAGTG 425
|||||
OY 181 ggcgtcgcgcagcttcacatcgtagtagtaaaaccccgcaactgtagcgcgccg 240
|||||
DB 426 GCGGCTCGCTGCAGACTTCATTCGCTAGTAGTAAACCCCGAATCGTACCGCGCC 485
|||||
OY 241 ggcgaagcgcgttaaaccccaactcttgatgtgacctcgatcagtaggaatacccg 300
|||||
DB 486 GGCCAAAGCGTTAAACCCCAACTTCTGAATGTGACCTCGATGAGTAAATACCGG 545
|||||
OY 301 ctgaactaa 310
|||||
DB 546 CTGAACCTTAA 555
|||||

RESULT 6
AF291061 596 bp DNA linear PLN 18-SEP-2001
LOCUS AF291061
DEFINITION Fusarium proliferatum NRRL 31071 18S ribosomal RNA, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2, complete sequence; 28S ribosomal RNA, partial sequence.
ACCESSION AF291061
VERSION AF291061.1 GI:15637128
KEYWORDS
SOURCE
ORGANISM Fusarium proliferatum.
Fusarium proliferatum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.
REFERENCE 1 (bases 1 to 596)
AUTHORS Kwon,S.-I., van Dohlon,C.D. and Anderson,A.J.
TITLE Gene sequence analysis of an opportunistic wheat pathogen, an isolate of Fusarium proliferatum
JOURNAL Can. J. Bot. 79 (9), 1115-1121 (2001)
REFERENCE 2 (bases 1 to 596)
AUTHORS Kwon,S.-I. and Anderson,A.J.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2000) Biology, Utah State University, Logan, UT 84322-5305, USA
LOCATION/Qualifiers

source 1..596
/organism="Fusarium proliferatum"
/strain="NRRL 31071"
/specific_host="Triticum aestivum cv. Super Dwarf"
/db_xref="taxon:42674"
<1..596
/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, 28S ribosomal RNA"
BASE COUNT 158 a 157 c 146 g 135 t
ORIGIN

Query Match 99.0% Score 306.8; DB 8; Length 596;
Best Local Similarity 99.4%; Pred. No. 4.9e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aatgcataagtaatggaatgcaaatcagtaataatcgaatcttgaacgcaca 60
|||||
DB 267 AATGCGATGAATGTAATGCAATTCAGAAATTCAGTAATCATCGAATCTTGAACGCACA 326
|||||
OY 61 ttgcgccgcagatattctgcgagcgatgcctgttcgagcgatcattcaaccctcaagcc 120
|||||
DB 327 TTGCGCCGCCAGTATTCGTGGCGGCAATGCCTGTTCGAGCGCTCATTTCAACCCCAAGCC 386
|||||
OY 121 cccgggttggtgttgaggatcggaacgacctgtgcgcaagcgcgcccgaaatcagtgtg 180
|||||
DB 387 CCCGGGTTGGTGTGGGGATCGCGAGCCCTTGCAGCAGCCGCCCGCAAACTCTAGTG 446
|||||
OY 181 ggcgtcgcgcagcttcacatcgtagtagtaaaacccctcgcaactgtagcgcgccg 240
|||||
DB 447 GCGGCTCGCTGCAGACTTCATTCGCTAGTAGTAAACCCCTGCAACTGTGTACGGCGGCC 506
|||||
OY 241 ggcgaagcgcgttaaaccccaactcttgatgttgcacctcgatcagtaggaatacccg 300
|||||
DB 507 GGCCAAAGCGTTAAACCCCAACTTCTGAATGTGACCTCGATGAGTAAATACCGG 566
|||||
OY 301 ctgaactaa 310
|||||
DB 567 CTGAACCTTAA 576
|||||

RESULT 7
AR168094 2293 bp DNA linear PAT 17-DEC-2001
LOCUS AR168094
DEFINITION Sequence 1 from patent US 6287800.
ACCESSION AR168094
VERSION AR168094.1 GI:17903914
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2293)
AUTHORS Gallazzo,J.L. and Lee,M.D.
TITLE Production of high titers of gibberellins, GA4 and GA7, by Gibberella fujikuroi strain LTB-1027
JOURNAL Patent: US 6287800-A 1 11-SEP-2001;
LOCATION/Qualifiers
source 1..2293
/organism="unknown"
BASE COUNT 596 a 527 c 592 g 578 t
ORIGIN

Query Match 99.0% Score 306.8; DB 6; Length 2293;
Best Local Similarity 99.4%; Pred. No. 5.8e-84;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aatgcataagtaatggaatgcaaatcagtaataatcgaatcttgaacgcaca 60
|||||
DB 1972 AATGCGATGAATGTAATGCAATTCAGAAATTCAGTAATCATCGAATCTTGAACGCACA 2031
|||||
OY 61 ttgcgccgcagatattctgcgagcgatgcctgttcgagcgatcattcaaccctcaagcc 120
|||||

Db	2032	TTGGCCCGCCAGTATCTGGGGGCGCATTCGCGAGCGTCAATTCACCCCTCAAGCC	2091
QY	121	cccgaggttggtgtgtggagatcgcgdaaaccccttggggagaacggccgggaatctagt	180
Db	2092	CCCGGGTTGGGTGGGGGATCGCGAGCCCTGCGGCAAGCGGCGCCGGAATCTAGTG	2151
QY	181	gcggtctcgctgcagctctccatctgcgtagtagtaaaacccctcgcaactgtaacgcygc	240
Db	2152	CGCGTCTGCGCTGCACCTTCACATTCGTAGTAGTAACACCTCGCAACGTACGCGCGCGC	2211
QY	241	ggccagacgcgttaaaaccccccaactcttaagtctgaactcgtgacatagtagtaataccg	300
Db	2212	GGCCAAAGCGTTAAACCCCAACTCTGAATGTTAAGCTCGGATAGGTAGGAATACCCG	2271
QY	301	ctgaacttaa	310
Db	2272	CTGAACCTTAA	2281

RESULT	8
LOCUS	AF158303
DEFINITION	AF158303 531 bp DNA linear PLN 21-MAR-2000
ACCESSION	Fusarium sp. NRRL26794 18S ribosomal RNA gene, partial sequence;
VERSION	Internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
KEYWORDS	transcribed spacer 2, complete sequence; and 28S ribosomal RNA
SOURCE	gene, partial sequence.
ORGANISM	AF158303
REFERENCE	AF158303.1 GI:7106206
AUTHORS	Fusarium sp. NRRL26794.
TITLE	Fusarium sp. NRRL26794.
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS	Hypocreales; mitosporic Hypocreales; Fusarium.
TITLE	1 (bases 1 to 531)
REFERENCE	O'Donnell, K., Nirenberg, H. I., Aoki, T. and Cigelsink, E.
AUTHORS	A multigene phylogeny of the Gibberella fujikuroi species complex:
TITLE	detection of additional phylogenetically distinct species
JOURNAL	Mycoscience 41, 61-78 (2000)
REFERENCE	2 (bases 1 to 531)
AUTHORS	O'Donnell, K.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUN-1999) Microbial Properties, NCUR-USDA-ARS, 1815
FEATURES	N. University St., Peoria, IL 61604, USA
SOURCE	Location/Qualifiers
	1..531
	/organism="Fusarium sp. NRRL26794"
	/strain="NRRL26794"
	/db_xref="taxon:100621"
	<1..23
rRNA	/product="18S ribosomal RNA"
misc_RNA	24..169
rRNA	/product="internal transcribed spacer 1"
misc_RNA	170..328
rRNA	/product="5.8S ribosomal RNA"
misc_RNA	329..493
rRNA	/product="internal transcribed spacer 2"
misc_RNA	494..531
rRNA	/product="28S ribosomal RNA"
BASE COUNT	137 a 146 c 128 g 120 t
ORIGIN	

Db	282	TTGGCCCGCAGTATTCCTGGGGGCGACATGCGTTTCGAGCGTCATTTCAACCCCTCAAGCC	341
Qy	121	cccgaggttgtagtggtgtagggatcgcgaagccctgcgcgaagccggccccgaatcagtg	180
Db	342	CTCGGGTTTGGTGTTGGGGGATCGGGACCCCTTGGCGCAACCCGGCCCCGAAATCTACTG	401
Qy	181	gcgcgtcgcgtgcagcttcacatctgcgtagtagtaaacccctgcgaactgtaacgcgcgc	240
Db	402	GCGGCTCTGGCTGCAGCTTCCATTGGCGTAGTAGTAANAACCTTCGCACACTGGTACGGGGCC	461
Qy	241	ggccaagccgctaaaccccccaactctcgaatcttgacctgcgatcaagtagaataaccg	300
Db	462	GGCCAAGCCGTTAAACCCCAACTCTGTAATGTTGACCTCGGATCAGGTAGGAATACCG	521
Qy	301	ctgaactaa 310	
Db	522	CTGAACCTTAA 531	

RESULT	9
AF158304	
LOCUS	540 bp DNA linear PLN 21-MAR-2000
DEFINITION	Fusarium sp. NRRL28852 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION	AF158304
VERSION	AF158304.1 GI:7106207
KEYWORDS	
SOURCE	.
ORGANISM	Fusarium sp. NRRL28852. Fusarium sp. NRRL28852. Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Microsporitic Hypocreales; Fusarium.
REFERENCE	1 (bases 1 to 540)
AUTHORS	O'Donnell,K., Nirenberg,H.I., Aoki,T. and Cigelnik,E.
TITLE	A multigenic phylogeny of the Gibberella fujikuroi species complex: detection of additional phylogenetically distinct species
JOURNAL	Mycoscience 41, 61-78 (2000)
REFERENCE	2 (bases 1 to 540)
AUTHORS	O'Donnell,K.
JOURNAL	Direct Submission Submitted (10-JUN-1999) Microbial Properties, NCUR-USDA-ARS, 1815 N. University St., Peoria, IL 61604, USA
FEATURES	Location/Qualifiers
SOURCE	1..540 /organism="Fusarium sp. NRRL28852" /strain="NRRL28852" /db_xref="taxon:100622" <1..32 /product="18S ribosomal RNA" 33..178 /product="internal transcribed spacer 1" 179..337 /product="5.8S ribosomal RNA" 338..502 /product="internal transcribed spacer 2" 503..>540 /product="28S ribosomal RNA"
RNA	
misc_RNA	
RNA	
misc_RNA	
BASE COUNT	137 a 151 c 130 g 122 t
ORIGIN	

	Query Match	98.5%	Score 305..2;	DB 8;	Length 531;
	Best Local Similarity	99.0%;	Pred. No. 1.5e-83;		
	Matches 307; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
Oy	1	aatgcgataagtaatcgtgaattcgaaataatcgaatgatcatcgaatttgaagccaca	60		
Db	222	AATCGGTAAGTAAATCGAATTGCAGAAATTCAGGAATCTCGAATTTTGAAAGCACA	281		
Oy	61	ttagccgcccaagatattctggcgggacatgacctgtttcgaagcatattcaacccttaagcc	120		

	Query Match	Score	305.2	DB 8	Length	540
	Best Local Similarity	99.0%	Pred.	1.5e-83		
	Matches	307	Conservative	0	Mismatches	3
					Indels	0
					Gaps	0
Qy	1	aaatgagtaagtaatgtgataatgcacaaatcgaatgatacatcgaaatcttgaacgcaca	60			
Db	231	AAATCGATTAAGTAATGTGAATGACGAAATTCAGATGATCATCGAATCTTTGAAACGCCA	290			
Qy	61	ttgcgccccgcagtaattcttgccgagcagacctgttctgcagcgtcaattcaaccctcaagcc	120			
Db	291	TTGCCTCCCGCCAGTTTGTGGCGGGCAGTCTGTGTGGAGCGTCAATTTCAACCTCAACCC	350			

OY 121 cccgggttggtgtgtggtggaatcggaagcccttcgagcaagccgccccgaatctagt 180
 |||||||
 Db 351 CCCGGGTTTGTTGGTGATCGCGAGCCCTCGCGCAAGCCGCCCCGAATCTAGTG 410
 OY 181 ggggttcgtcgcagcttcacatcgttagtagtaaaacccctcgcaactgtagcgagc 240
 |||||||
 Db 411 GCGGTCTCGCTGAGCTTCATTCGTAGTAGTAACCCCTCGCAACTGTAGCGGCGC 470
 OY 241 ggcgaagccgttaaaccccccaacttcgtatgttgacctcgatcgatgtaataccg 300
 |||||||
 Db 471 GGCCAAGCCGTTAAACCCCAACTTCGATGTGACCTCGGATCAGTAGAATACCCG 530
 OY 301 ctgaactaa 310
 |||||||
 Db 531 CTGAACCTTAA 540

RESULT 10
 AF158302 540 bp DNA linear PLN 21-MAR-2000
 LOCUS
 DEFINITION Fusarium sp. NRRL26427 18S ribosomal RNA gene, partial sequence;
 internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 28S ribosomal RNA
 gene, partial sequence.
 ACCESSION AF158302
 VERSION AF158302.1 GI:7106205
 KEYWORDS
 SOURCE Fusarium sp. NRRL26427.
 ORGANISM Fusarium sp. NRRL26427
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 540)
 O'Donnell, K., Nirenberg, H. I., Aoki, T. and Cigelnik, E.
 A multigene phylogeny of the Gibberella fujikuroi species complex:
 detection of additional phylogenetically distinct species
 Mycoscience 41, 61-78 (2000)
 REFERENCE 2 (bases 1 to 540)
 O'Donnell, K.
 Direct Submission
 Submitted (10-JUN-1999) Microbial Properties, NCAR-USDA-ARS, 1815
 University St., Peoria, IL 61604, USA
 JOURNAL Location/Qualifiers
 FEATURES
 source 1..540
 /organism="Fusarium sp. NRRL26427"
 /strain="NRRL26427"
 /db_xref="taxon:100620"
 <1..32
 rRNA /product="18S ribosomal RNA"
 33..178
 misc_RNA /product="internal transcribed spacer 1"
 179..337
 rRNA /product="5.8S ribosomal RNA"
 338..502
 misc_RNA /product="internal transcribed spacer 2"
 503..>540
 rRNA /product="28S ribosomal RNA"
 BASE COUNT 137 a 150 c 130 g 123 t
 ORIGIN

Query Match 97.9% Score 303.6; DB 8; Length 540;
 Best Local Similarity 98.7% Pred. No. 4.7e-83;
 Matches 306; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 1 aatgcatgaatgaatgtaattgcaaaatcagtgatcatcgaatcttgaagcaca 60
 |||||||
 Db 231 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATGCAATCTTGAACGACA 290
 OY 61 ttggccgcgcagatattcttgcggagcctgcctgttcgagcgatcattcaaccctaaagc 120
 |||||||
 Db 291 TTGCGCCCGCAGTAATTCGCGGCGCATGCTGTTCAGGCGTCAATTCACCCCTCAAGCC 350

OY 121 cccgggttggtgtgtggtggaatcggaagcccttcgagcaagccgccccgaatctagt 180
 |||||||
 Db 351 CCCGGGTTTGTTGGTGATCGCGAGCCCTCGCGCAAGCCGCCCCGAATCTAGTG 410
 OY 181 ggggttcgtcgcagcttcacatcgttagtagtaaaacccctcgcaactgtagcgagc 240
 |||||||
 Db 411 GCGGTCTCGCTGAGCTTCATTCGTAGTAGTAACCCCTCGCAACTGTAGCGGCGC 470
 OY 241 ggcgaagccgttaaaccccccaacttcgtatgttgacctcgatcgatgtaataccg 300
 |||||||
 Db 471 GGCCAAGCCGTTAAACCCCAACTTCGATGTGACCTCGGATCAGTAGAATACCCG 530
 OY 301 ctgaactaa 310
 |||||||
 Db 531 CTGAACCTTAA 540

RESULT 11
 FEU34557
 LOCUS
 DEFINITION Fusarium fujikuroi internal transcribed spacer RNA.
 ACCESSION U34557
 VERSION U34557.1 GI:1808928
 KEYWORDS
 SOURCE Gibberella fujikuroi.
 ORGANISM Gibberella fujikuroi.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; Nectriaceae; Gibberella; Gibberella fujikuroi complex.

REFERENCE 1 (bases 1 to 534)
 O'Donnell, K. and Cigelnik, E.
 Two divergent intragenomic rDNA ITS2 types within a monophyletic
 lineage of the fungus Fusarium are nonorthologous
 Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
 JOURNAL Mol. Phylogenet. Evol. 7 (1), 103-116 (1997)
 REFERENCE 2 (bases 1 to 534)
 O'Donnell, K., Cigelnik, E. and Nirenberg, H. I.
 Molecular systematics and phylogeography of the Gibberella
 fujikuroi species complex
 Mycologia 90 (3), 465-493 (1998)
 REFERENCE 3 (bases 1 to 534)
 O'Donnell, K. and Cigelnik, E.
 Direct Submission
 Submitted (21-AUG-1995) Kerry O'Donnell, NCAR, USDA, 1815 N.
 University St., Peoria, IL 61604, USA
 JOURNAL Location/Qualifiers
 FEATURES
 source 1..534
 /organism="Gibberella fujikuroi"
 /strain="NRRL 13566"
 /db_xref="taxon:5127"
 1..534
 misc_RNA /product="internal transcribed spacer"
 BASE COUNT 135 a 149 c 130 g 120 t
 ORIGIN

Query Match 97.7% Score 302.8; DB 8; Length 534;
 Best Local Similarity 99.3% Pred. No. 8.4e-83;
 Matches 304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 aatgcatgaatgaatgtaattgcaaaatcagtgatcatcgaatcttgaagcaca 60
 |||||||
 Db 229 AATGCGATTAAGTAATGTAATTCAGAAATTCAGTAATCATGCAATCTTGAACGACA 288
 OY 61 ttggccgcgcagatattcttgcggagcctgcctgttcgagcgatcattcaaccctaaagc 120
 |||||||
 Db 289 TTGCGCCCGCAGTAATTCGCGGCGCATGCTGTTCGAGCGTCAATTCACCCCTCAAGCC 348
 OY 121 cccgggttggtgtgtggtggaatcggaagcccttcgagcaagccgccccgaatctagt 180
 |||||||
 Db 349 CCCGGGTTTGTTGGTGATCGCGAGCCCTTCGCGCAAGCCGCCCCGAATCTAGTG 408
 OY 181 ggggttcgtcgcagcttcacatcgttagtagtaaaacccctcgcaactgtagcgagc 240
 |||||||


```
RESULT 8
US-08-737-129A-5/C
: Sequence 5, Application US/08737129A
: Patent No. 5885816
: GENERAL INFORMATION:
: APPLICANT: Ikao FUJII et al.
: TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
: TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Menderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/737,129A
: FILING DATE: No. 5885816member 15, 1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warren M. Cheek, Jr.
: REGISTRATION NUMBER: 33,367
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-8850
: TELEFAX:
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 666 bases
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-737-129A-5

Query Match 77.8%; Score 14; DB 2; Length 666;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||
DB 596 GTGACGCTCTCGCT 583

RESULT 9
PCT-US94-14106-58/C
: Sequence 58, Application PC/TUS9414106
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Process for Generating Specific Antibodies
: NUMBER OF SEQUENCES: 61
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14106
: FILING DATE:
: CLASSIFICATION:
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: INFORMATION FOR SEQ ID NO: 58:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 717 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 67..717
: PCT-US94-14106-58

Query Match 77.8%; Score 14; DB 5; Length 717;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||
DB 653 GTGACGCTCTCGCT 640
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```
RESULT 10
PCT-US94-14106-50/C
: Sequence 50, Application PC/TUS9414106
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Process for Generating Specific Antibodies
: NUMBER OF SEQUENCES: 61
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/14106
: FILING DATE:
: CLASSIFICATION:
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 735 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 67..735
: PCT-US94-14106-50

Query Match 77.8%; Score 14; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||
DB 671 GTGACGCTCTCGCT 658

RESULT 11
PCT-US94-14106-54/C
: Sequence 54, Application PC/TUS9414106
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Process for Generating Specific Antibodies
: NUMBER OF SEQUENCES: 61
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..735
PCT-US94-14106-54

Query Match 77.8%; Score 14; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||

Db 671 GTGACGCTCGCT 658

RESULT 12
US-08-860-882A-25/c
Sequence 25, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAW, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HOW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-25

Query Match 77.8%; Score 14; DB 2; Length 777;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||

Db 677 GTGACGCTCGCT 664

RESULT 13
US-08-133-011-99/c
Sequence 99, Application US/08133011
Patent No. 5658727
GENERAL INFORMATION:
APPLICANT: Kang, Andray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,011
FILING DATE: 08-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-133-011-99

Query Match 77.8%; Score 14; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacggtctcgct 18
|||||

Db 695 GTGACGCTCGCT 682

RESULT 14

US-08-322-730A-99/C
Sequence 99, Application US/08322730A
Patent No. 5759817

GENERAL INFORMATION:

APPLICANT: Bardas, Carlos

TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10550 No. 5759817th Torrey Pines Road, Suite 220,

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/322,730A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/826,623

FILING DATE: 27-JAN-1992

APPLICATION NUMBER: US 07/683,602

FILING DATE: 10-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bingham, Douglas A

REGISTRATION NUMBER: 32,457

REFERENCE/DOCKET NUMBER: SCRO707P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-784-2937

TELEFAX: 619-784-9399

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:

LENGTH: 798 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-322-730A-99

Query Match 77.8%; Score 14; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacgctcgcct 18

|||||

Db 695 GTGACGCTCGCT 682

RESULT 15

US-08-387-874-71/C

Sequence 71, Application US/08387874

Patent No. 5770356

GENERAL INFORMATION:

APPLICANT: Light, Paul L., II

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: PHAGEMIDS COEXPRESSING A SURFACE

RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,874

FILING DATE: 22-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08364

FILING DATE: 03-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,369

FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 303.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-6312

TELEFAX: 619-554-2937

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 798 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-387-874-71

Query Match 77.8%; Score 14; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgacgctcgcct 18

|||||

Db 695 GTGACGCTCGCT 682

Search completed: August 21, 2002, 22:12:29
Job time: 5702 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:39:29 ; Search time 8184.59 Seconds
(without alignments)
47.581 Million cell updates/sec

Title: US-10-046-955-49
Perfect score: 18
Sequence: 1 tctagtgacggtctgcgt 18

Scoring table:
IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	18	100.0	18	US-09-423-233-49	Sequence 49, Appl
2	16.4	91.1	310	US-09-423-233-7	Sequence 7, Appl1
3	16.4	91.1	534	US-09-961-7554-7	Sequence 7, Appl1
4	16.4	91.1	637	US-09-580-797-12	Sequence 12, Appl
5	15.4	85.6	218	US-09-270-849B-60978	Sequence 60978, A
6	15.4	85.6	279	US-09-394-745-22526	Sequence 22526, A
7	15.4	85.6	279	US-09-565-306-46194	Sequence 46194, A
8	15.4	85.6	279	US-09-654-617-323951	Sequence 323951, A
9	15.4	85.6	279	US-09-684-016-323951	Sequence 323951, A
10	15.4	85.6	443	US-09-270-849B-105057	Sequence 105057, A
11	15.4	85.6	592	US-09-505-532-22896	Sequence 22896, A
12	15.4	85.6	592	US-09-819-091A-22896	Sequence 22896, A
13	15.4	85.6	744	US-09-708-427-6695	Sequence 6695, A
14	15.4	85.6	879	US-09-270-849B-124742	Sequence 124742, A
15	15.4	85.6	1123	US-09-620-392-4174	Sequence 139165, A
16	15.4	85.6	7555	US-09-620-392-10798	Sequence 10798, A
17	15.4	85.6	9852	US-09-620-392-10798	Sequence 10798, A
18	15.4	85.6	14744	US-09-702-134-4847	Sequence 4847, A
19	15.4	85.6	14744	US-09-815-264-82429	Sequence 82429, A
20	15.4	85.6	78341	US-09-534-859-4	Sequence 4, Appl1
21	15.4	85.6	78341	US-09-803-736-4	Sequence 4, Appl1
22	15	83.3	143	US-09-342-217-2185	Sequence 2185, A
23	15	83.3	143	US-09-342-217-2185	Sequence 2185, A
24	15	83.3	241	US-08-728-362-1069	Sequence 1069, A
25	15	83.3	241	US-08-992-332-1069	Sequence 1069, A
26	15	83.3	241	US-60-005-019-1069	Sequence 1069, A
27	15	83.3	242	US-09-250-152-2676	Sequence 2676, A
28	15	83.3	245	US-08-330-011-2992	Sequence 2992, A
29	15	83.3	245	US-08-440-743-1546	Sequence 1546, A
30	15	83.3	245	US-09-540-229-91070	Sequence 91070, A
31	15	83.3	249	US-09-540-229-116567	Sequence 116567, A

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C 32 15 83.3 255 21 US-09-540-229-106380 Sequence 106380,
C 33 15 83.3 264 20 US-09-539-806-41390 Sequence 41390, A
C 34 15 83.3 277 21 US-09-540-229-114380 Sequence 114380,
C 35 15 83.3 277 21 US-09-540-766-58240 Sequence 58240, A
C 36 15 83.3 280 17 US-09-321-214-18008 Sequence 18008, A
C 37 15 83.3 280 19 US-09-516-335-18008 Sequence 18008, A
C 38 15 83.3 280 29 US-09-733-811-18008 Sequence 18008, A
C 39 15 83.3 280 29 US-09-733-811A-18008 Sequence 18008, A
C 40 15 83.3 280 36 US-09-975-640-18008 Sequence 18008, A
C 41 15 83.3 280 36 US-09-975-640A-18008 Sequence 18008, A
C 42 15 83.3 281 21 US-09-540-764-49406 Sequence 49406, A
C 43 15 83.3 293 5 US-08-196-363-4820 Sequence 4820, Ap
C 44 15 83.3 293 5 US-08-196-363A-4820 Sequence 4820, Ap
C 45 15 83.3 293 5 US-08-196-363-4820 Sequence 4820, Ap
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ALIGNMENTS

```
RESULT 1
US-09-423-233-49
; Sequence 49, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-49
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 18; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 tctagtgcggtctcgct 18
    |||
Db 1 tctagtgcggtctcgct 18

RESULT 2
US-09-423-233-7
; Sequence 7, Application US/09423233
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-09-423-233-7
```

```
Query Match
Best Local Similarity 94.4%; Score 16.4; DB 18; Length 310;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 tctagtgcggtctcgct 18
    |||
Db 174 tctagtgcggtctcgct 191
```

```
RESULT 3
US-09-961-755A-7
; Sequence 7, Application US/09961755A
; GENERAL INFORMATION:
; APPLICANT: Barnett, Jason
; TITLE OF INVENTION: Detection of Fusarium Species Infecting Corn Using the
; FILE REFERENCE: 60055
; CURRENT APPLICATION NUMBER: US/09/961,755A
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Fusarium proliferatum
US-09-961-755A-7
```

```
Query Match
Best Local Similarity 94.4%; Score 16.4; DB 36; Length 534;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 tctagtgcggtctcgct 18
    |||
Db 402 tctagtgcggtctcgct 419
```

```
RESULT 4
US-09-580-797-12
; Sequence 12, Application US/09580797
; GENERAL INFORMATION:
; APPLICANT: Iwen, Peter C.
; APPLICANT: Hinrichs, Steven H.
; APPLICANT: Henry, Travis
; TITLE OF INVENTION: Board of Regents of the University of Nebraska
; TITLE OF INVENTION: Materials and Methods for Molecular
; FILE REFERENCE: UNMC 63149
; CURRENT APPLICATION NUMBER: US/09/580,797
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Fusarium moniliformes
US-09-580-797-12
```

```
Query Match
Best Local Similarity 91.1%; Score 16.4; DB 22; Length 637;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 tctagtgcggtctcgct 18
    |||
Db 514 tctagtgcggtctcgct 531
```

```
RESULT 5
US-09-270-849B-60978
; Sequence 60978, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 60978
; LENGTH: 218
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-60978
```

```
Query Match      85.6%; Score 15.4; DB 16; Length 218;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2 ctatgacggtctcgct 18
        ||| ||| ||| ||| |||
DB      41 ctatgacggtctcgct 57
```

```
RESULT 6
US-09-394-745-22526
; Sequence 22526, Application US/09394745
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15454)B
; CURRENT APPLICATION NUMBER: US/09/394,745
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 57264
; SEQ ID NO 22526
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3066-031-Q1-E1-F12
US-09-394-745-22526
```

```
Query Match      85.6%; Score 15.4; DB 17; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 ctatgacggtctcgct 18
        | ||| ||| ||| ||| |||
DB      82 cgagtgacggtctcgct 98
```

```
RESULT 7
US-09-565-306-46194
; Sequence 46194, Application US/09565306
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15459)C
; CURRENT APPLICATION NUMBER: US/09/565,306
; CURRENT FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 46194
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3066-031-Q1-E1-F12
US-09-565-306-46194
```

```
Query Match      85.6%; Score 15.4; DB 22; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2 ctatgacggtctcgct 18
```

```
DB      82 cgagtgacggtctcgct 98
```

```
RESULT 8
US-09-654-617-323951
; Sequence 323951, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 323951
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
US-09-654-617-323951
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```
Query Match      85.6%; Score 15.4; DB 25; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 ctatgacggtctcgct 18
        | ||| ||| ||| ||| |||
DB      82 cgagtgacggtctcgct 98
```

```
RESULT 9
US-09-684-016-323951
; Sequence 323951, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 323951
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Zea mays
US-09-684-016-323951
```

```
Query Match      85.6%; Score 15.4; DB 27; Length 279;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 ctatgacggtctcgct 18
        | ||| ||| ||| ||| |||
DB      82 cgagtgacggtctcgct 98
```

```
RESULT 10
US-09-270-849B-105057
; Sequence 105057, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105057
; LENGTH: 443
```

```
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-105057
```

```
Query Match      85.6%: Score 15.4; DB 16: Length 443;
Best Local Similarity 94.1%: Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 tctagtacggtctcgc 17
         ||||| ||||| |||||
DB      253 tctagtacggtctcgc 269
```

```
RESULT 11
US-09-505-532-22896
Sequence 22896, Application US/09505532
```

```
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15478)B
CURRENT APPLICATION NUMBER: US/09/505,532
PRIOR FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
NUMBER OF SEQ ID NOS: 51470
SEQ ID NO 22896
LENGTH: 592
TYPE: DNA
ORGANISM: Arabidopsis thaliana columbia
OTHER INFORMATION: unsure at all n locations
US-09-505-532-22896
```

```
Query Match      85.6%: Score 15.4; DB 19: Length 592;
Best Local Similarity 94.1%: Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctagtacggtctcgc 18
         ||||| ||||| |||||
DB      201 ctagtacggtctcgc 217
```

```
RESULT 12
US-09-819-091A-22896
Sequence 22896, Application US/09819091A
```

```
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15478)B
CURRENT APPLICATION NUMBER: US/09/819,091A
CURRENT FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: US 60/108,420
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: US 60/120,645
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 09/443,025
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 51470
SEQ ID NO 22896
LENGTH: 592
TYPE: DNA
ORGANISM: Arabidopsis thaliana columbia
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(592)
OTHER INFORMATION: unsure at all n locations
US-09-819-091A-22896
```

```
Query Match      85.6%: Score 15.4; DB 31: Length 592;
Best Local Similarity 94.1%: Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctagtacggtctcgc 18
         ||||| ||||| |||||
DB      201 ctagtacggtctcgc 217
```

```
RESULT 13
US-09-708-427-6695
Sequence 6695, Application US/09708427
```

```
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6695
LENGTH: 744
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..744
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc.feature
LOCATION: 1..744
OTHER INFORMATION: Ceres Seq. ID 1816224
US-09-708-427-6695
```

```
Query Match      85.6%: Score 15.4; DB 28: Length 744;
Best Local Similarity 94.1%: Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctagtacggtctcgc 18
         ||||| ||||| |||||
DB      218 ctagtacggtctcgc 234
```

```
RESULT 14
```

```
US-09-270-849B-124742/C
Sequence 124742, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 124742
LENGTH: 879
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-124742
```

```
Query Match      85.6%: Score 15.4; DB 16: Length 879;
Best Local Similarity 94.1%: Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 ctagtacggtctcgc 18
         ||||| ||||| |||||
DB      482 ctagtacggtctcgc 466
```

```

RESULT 15
US-09-270-849B-139165/C
; Sequence 139165, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/270,849B
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 195450
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139165
; LENGTH: 1123
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-139165

```

```

Query Match 85.6%; Score 15.4; DB 16; Length 1123;
Best Local Similarity 94.1%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ctatgtacggtctcgt 18
1 |||
DB 279 CGAGTCACGCTCTCGCT 263

```

Search completed: August 22, 2002, 00:39:32
Job time: 13057 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2002, 00:50:50 ; Search time 663.62 Seconds
(without alignments)
72,981 Million cell updates/sec

Title: US-10-046-955-49

Perfect score: 1 tctagtacgctcgcgt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1721111 seqs, 1345317543 residues

Total number of hits satisfying chosen parameters: 3442222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/pdata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/pdata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/pdata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/pdata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/pdata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/pdata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/pdata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/pdata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	7	US-10-046-955-49
2	16.4	91.1	310	7	US-10-046-955-7
3	15	83.3	386	5	US-09-918-995-33508
4	15	83.3	446	5	US-09-918-995-34287
5	15	83.3	473	5	US-09-918-995-1024
6	15	83.3	1624	5	US-09-919-002-3535
7	14.8	82.2	403	5	US-09-785-276A-2782
8	14.8	82.2	599	7	US-10-027-632-215234
9	14.8	82.2	599	7	US-10-027-632-215235
10	14.8	82.2	1192	6	US-10-098-754-3118
11	14.8	82.2	1549	5	US-09-634-754C-156
12	14.8	82.2	1549	5	US-09-634-754D-156
13	14.8	82.2	25593	1	PCT-US02-14011-1
14	14.8	82.2	277	5	US-09-539-331D-39667
15	14.8	82.2	295	5	US-09-540-210B-17019
16	14.8	77.8	736	7	US-10-006-773-12
17	14.8	77.8	1666	6	US-10-098-754-10959
18	14.8	77.8	1800	7	US-10-170-155-6
19	14.8	77.8	2140	1	PCT-US02-22866-42
20	14.8	77.8	4191	7	US-10-176-380-18
21	14.8	77.8	5691	5	US-09-897-511A-11
22	14.8	77.8	5711	5	US-09-897-511A-8
23	14.8	77.8	6255	5	US-09-887-511A-13
24	13.8	76.7	25	5	US-09-396-196G-117408
25	13.8	76.7	220	7	US-10-137-316-56

26	13.8	76.7	309	5	US-09-540-210B-34640	Sequence 34640, A
27	13.8	76.7	319	7	US-10-137-316-10	Sequence 10, Appl
28	13.8	76.7	319	7	US-10-137-316-40	Sequence 40, Appl
29	13.8	76.7	371	5	US-09-785-276A-12650	Sequence 12650, A
30	13.8	76.7	373	5	US-09-785-276A-3481	Sequence 3481, Ap
31	13.8	76.7	383	5	US-09-785-276A-11609	Sequence 11609, A
32	13.8	76.7	384	5	US-09-785-276A-11951	Sequence 11951, A
33	13.8	76.7	403	5	US-09-785-276A-10948	Sequence 10948, A
34	13.8	76.7	410	5	US-09-785-276A-37090	Sequence 37090, A
35	13.8	76.7	410	5	US-09-785-276A-41707	Sequence 41707, A
36	13.8	76.7	413	5	US-09-785-276A-12666	Sequence 12666, A
37	13.8	76.7	413	5	US-09-785-276A-33807	Sequence 33807, A
38	13.8	76.7	415	5	US-09-785-276A-7121	Sequence 7121, Ap
39	13.8	76.7	418	5	US-09-785-276A-32781	Sequence 32781, A
40	13.8	76.7	419	5	US-09-785-276A-33123	Sequence 33123, A
41	13.8	76.7	419	5	US-09-785-276A-42049	Sequence 42049, A
42	13.8	76.7	420	5	US-09-785-276A-2440	Sequence 2440, Ap
43	13.8	76.7	432	7	US-10-137-316-27	Sequence 27, Appl
44	13.8	76.7	443	5	US-09-785-276A-32125	Sequence 32125, A
45	13.8	76.7	443	5	US-09-785-276A-40220	Sequence 40220, A

ALIGNMENTS

RESULT 1
US-10-046-955-49
Sequence 49, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.
APPLICANT: Reis, Errol
APPLICANT: Aldorovich, Lilliana
TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
FILE REFERENCE: 6395-62064
CURRENT APPLICATION NUMBER: US/10/046,955
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 09/423,233
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: PCT/US98/08926
PRIOR FILING DATE: 1998-05-01
PRIOR APPLICATION NUMBER: US 60/045,400
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 18
TYPE: DNA
ORGANISM: Fusarium moniliforme
US-10-046-955-49

Query Match 100.0%; Score 18; DB 7; Length 18;
Best local Similarity 100.0%; Pred. NO. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctagtacgctcgcgt 18
|||||
Db 1 tctagtacgctcgcgt 18

RESULT 2
US-10-046-955-7
Sequence 7, Application US/10046955
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as Represented by the
APPLICANT: Secretary of the Department of Health and Human Services, Centers for
APPLICANT: Control and Prevention
APPLICANT: Morrison, Christine J.

```
; APPLICANT: Reiss, Errol
; APPLICANT: Aidorevich, Lilliana
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 6395-62064
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/423,233
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: PCT/US98/08926
; PRIOR FILING DATE: 1998-05-01
; PRIOR APPLICATION NUMBER: US 60/045,400
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: DNA
; ORGANISM: Fusarium moniliforme
US-10-046-955-7
```

```
Query Match          91.1%; Score 16.4; DB 7; Length 310;
Best Local Similarity 94.4%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 tctagtgcggtctgcgt 18
Db 174 tctagtgcggtctgcgt 191
```

```
RESULT 3
US-09-918-995-33508/c
; Sequence 33508, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33508
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33508
```

```
Query Match          83.3%; Score 15; DB 5; Length 386;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 agtgacggtctgcgt 18
Db 208 agtgacggtctgcgt 194
```

```
RESULT 4
US-09-918-995-34287/c
; Sequence 34287, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 076
```

```
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34287
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-34287
```

```
Query Match          83.3%; Score 15; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 agtgacggtctgcgt 18
Db 253 agtgacggtctgcgt 239
```

```
RESULT 5
US-09-918-995-1024/c
; Sequence 1024, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1024
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1024
```

```
Query Match          83.3%; Score 15; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 agtgacggtctgcgt 18
Db 230 agtgacggtctgcgt 216
```

```
RESULT 6
US-09-919-002-3555
; Sequence 3555, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
```

```
SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 3555
: LENGTH: 1624
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-919-002-3555
```

```
Query Match      83.3%  Score 15:  DB 5:  Length 1624;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15:  Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      4 agtgcagctcgcct 18
      |||
Db      1387 agtgcagctcgcct 1401
```

```
RESULT 7
US-09-785-276A-2782/c
: Sequence 2782, Application US/09785276A
```

```
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Endege, Wilson
```

```
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
: TITLE OF INVENTION: HUMAN PROSTATE CANCER
```

```
: FILE REFERENCE: MRI-007B
: CURRENT APPLICATION NUMBER: US/09/785, 276A
: CURRENT FILING DATE: 2001-02-16
```

```
: PRIOR APPLICATION NUMBER: 60/183,319
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/189,862
```

```
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: 60/207,454
: PRIOR FILING DATE: 2000-05-25
```

```
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: 60/219,007
```

```
: PRIOR FILING DATE: 2000-07-18
: PRIOR APPLICATION NUMBER: 60/255,281
: PRIOR FILING DATE: 2000-12-13
```

```
: NUMBER OF SEQ ID NOS: 62232
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2782
```

```
: LENGTH: 403
: TYPE: DNA
: ORGANISM: Homo sapiens
```

```
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 211_216, 362, 364
```

```
: OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-2782
```

```
Query Match      82.2%  Score 14.8;  DB 5:  Length 403;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16:  Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 tctagtgcagctcgcct 18
      |||
Db      350 tctagtgcagctcgcct 333
```

```
RESULT 8
US-10-027-632-215234
: Sequence 215234, Application US/10027632
```

```
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027, 632
```

```
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218, 006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198, 676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193, 483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185, 218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167, 363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156, 358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146, 002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 215234
: LENGTH: 599
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-215234
```

```
Query Match      82.2%  Score 14.8;  DB 7:  Length 599;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16:  Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 tctagtgcagctcgcct 18
      |||
Db      206 tctagtgcagctcgcct 223
```

```
RESULT 9
US-10-027-632-215235
: Sequence 215235, Application US/10027632
```

```
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
```

```
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027, 632
: CURRENT FILING DATE: 2002-04-30
```

```
: PRIOR APPLICATION NUMBER: US 60/218, 006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198, 676
```

```
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193, 483
: PRIOR FILING DATE: 2000-03-29
```

```
: PRIOR APPLICATION NUMBER: US 60/185, 218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167, 363
```

```
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156, 358
: PRIOR FILING DATE: 1999-09-28
```

```
: PRIOR APPLICATION NUMBER: US 60/146, 002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 215235
: LENGTH: 599
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-215235
```

```
Query Match      82.2%  Score 14.8;  DB 7:  Length 599;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16:  Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 tctagtgcagctcgcct 18
      |||
Db      206 tctagtgcagctcgcct 223
```



```
RESULT 10
US-10-098-754-3118
; Sequence 3118, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
; APPLICANT: Ramachandran, Rakesh
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: ATX-001CN
; CURRENT APPLICATION NUMBER: US/10/098,754
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIORITY FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 2107
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3118
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1192)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-3118

Query Match      82.2%; Score 14.8; DB 6; Length 1192;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctagtgcagctcgcgt 18
||||| ||| ||| ||| |||
DB 748 tctagtgcagctcgcgt 765

RESULT 11
US-09-634-754C-156/C
; Sequence 156, Application US/09634754C
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/09/634,754C
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
; SEQ ID NO 156
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2822724CT1
; PUBLICATION INFORMATION:
US-09-634-754C-156

Query Match      82.2%; Score 14.8; DB 5; Length 1549;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctagtgcagctcgcgt 18
||||| ||| ||| ||| |||
DB 343 tctagtgcagctcgcgt 326
```

```
RESULT 12
US-09-634-754D-156/C
; Sequence 156, Application US/09634754D
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/09/634,754D
; CURRENT FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
; SEQ ID NO 156
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2822724CT1
; PUBLICATION INFORMATION:
US-09-634-754D-156

Query Match      82.2%; Score 14.8; DB 5; Length 1549;
Best Local Similarity 88.9%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tctagtgcagctcgcgt 18
||||| ||| ||| ||| |||
DB 343 tctagtgcagctcgcgt 326

RESULT 13
PCT-US02-14011-1/C
; Sequence 1, Application PCT/US0214011
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshy, Beena
; APPLICANT: Sankar, Angela
; APPLICANT: Sankar, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRA GENE
; FILE REFERENCE: MMH-0838PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14011
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/288,475
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 25593
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (7648)..(7648)
; OTHER INFORMATION: PS1: polymorphic base cytosine or thymine
; FEATURE:
; NAME/KEY: allele
; LOCATION: (7685)..(7685)
; OTHER INFORMATION: PS2: polymorphic base adenine or cytosine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12702)..(12801)
; OTHER INFORMATION: N's represent breaks between Genaisance Reference Nos. 468376
; FEATURE:
```

```
NAME/KEY: allele
LOCATION: (14001)..(14001)
OTHER INFORMATION: PS3: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15098)..(15197)
OTHER INFORMATION: N's represent breaks between GenAssance Reference Nos. 4683871 &
OTHER INFORMATION: 4683825
FEATURE:
NAME/KEY: allele
LOCATION: (15759)..(15759)
OTHER INFORMATION: PS4: polymorphic base guanine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (16071)..(16071)
OTHER INFORMATION: PS5: polymorphic base cytosine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (16077)..(16077)
OTHER INFORMATION: PS6: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (16124)..(16124)
OTHER INFORMATION: PS7: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16521)..(16620)
OTHER INFORMATION: N's represent breaks between GenAssance Reference Nos. 4683825 &
OTHER INFORMATION: 4683835
FEATURE:
NAME/KEY: allele
LOCATION: (17688)..(17688)
OTHER INFORMATION: PS8: polymorphic base thymine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (17989)..(17989)
OTHER INFORMATION: PS9: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18377)..(18377)
OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18417)..(18417)
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NAME/KEY: misc_feature
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OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18469)..(18469)
OTHER INFORMATION: N represents an unknown nucleotide
FEATURE:
NAME/KEY: allele
LOCATION: (20395)..(20395)
OTHER INFORMATION: PS10: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (20488)..(20488)
OTHER INFORMATION: PS11: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
LOCATION: (20542)..(20542)
OTHER INFORMATION: PS12: polymorphic base guanine or adenine
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NAME/KEY: allele
LOCATION: (20779)..(20779)
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FEATURE:
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LOCATION: (21779)..(21878)
OTHER INFORMATION: N's represent breaks between GenAssance Reference Nos. 4683835
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NAME/KEY: allele
LOCATION: (22016)..(22016)
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NAME/KEY: allele
LOCATION: (22040)..(22040)
OTHER INFORMATION: PS15: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (22076)..(22076)
OTHER INFORMATION: PS16: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (22090)..(22090)
OTHER INFORMATION: PS17: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (22117)..(22117)
OTHER INFORMATION: PS18: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (22320)..(22320)
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FEATURE:
NAME/KEY: allele
LOCATION: (24434)..(24434)
OTHER INFORMATION: PS20: polymorphic base guanine or adenine
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NAME/KEY: allele
LOCATION: (24462)..(24462)
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FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: (24824)..(24824)
OTHER INFORMATION: PS24: polymorphic base adenine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (24917)..(24917)
OTHER INFORMATION: PS25: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
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OTHER INFORMATION: PS26: polymorphic base guanine or adenine
FEATURE:
NAME/KEY: allele
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PCT-US02-14011-1

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Best Local Similarity  88.9%  Pred No. 1.4e+02;
Matches  16;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

QY      1  tctagtacggtctcgct 18
        ||||| 1 |||||11
Db      6169  TCTAGTGCTGCTCGCT 6152

RESULT  14
US-09-539-331D-39667/c
; Sequence 39667, Application US/09539331D
; GENERAL INFORMATION:
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: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
: FILE REFERENCE: PD-1022 CIP
: CURRENT APPLICATION NUMBER: US/09/539,331D
: PRIOR FILING DATE: 2000-03-30
: PRIOR APPLICATION REMOVED - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 40961
: SOFTWARE: PERL Program
: SEQ ID NO 39667
: LENGTH: 277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: Incyte ID No: hu00747836
: FEATURE:
: NAME/KEY: unuse
: LOCATION: 26, 38, 55, 70, 111, 124, 126, 128, 134, 147, 150-151, 168, 171, 189,
: LOCATION: 191, 209, 235, 238, 241, 258, 275
: OTHER INFORMATION: a, t, c, g, or other
: US-09-539-331D-39667

Query Match      77.8% Score 14; DB 5; Length 277;
Best Local Similarity 93.3% Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 agtcagcggctcgcct 18
DB 37 ACTGACGGCTGCTGCT 23

RESULT 15
US-09-540-210B-17019/c
: Sequence 17019, Application US/09540210B
: GENERAL INFORMATION:
: APPLICANT: Seilhamer, Jeffrey J.
: APPLICANT: Delegeane, Angelo M.
: APPLICANT: Stuart, Susan G.
: APPLICANT: Stuve, Laura L.
: APPLICANT: Mullahy, Sara J.
: APPLICANT: Naughton, Rebecca E.
: TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
: FILE REFERENCE: PD-1037 CIP
: CURRENT APPLICATION NUMBER: US/09/540,210B
: CURRENT FILING DATE: 2002-04-03
: PRIOR APPLICATION NUMBER: 08/972,899
: PRIOR FILING DATE: November 18, 1997
: PRIOR APPLICATION NUMBER: 08/395,244
: PRIOR FILING DATE: February 27, 1995
: PRIOR APPLICATION NUMBER: 08/722,922
: PRIOR FILING DATE: September 27, 1996
: PRIOR APPLICATION NUMBER: 60/005,526
: PRIOR FILING DATE: September 29, 1995
: PRIOR APPLICATION NUMBER: 08/824,029
: PRIOR FILING DATE: March 25, 1997
: PRIOR APPLICATION NUMBER: 60/014,010
: PRIOR FILING DATE: March 25, 1996
: PRIOR APPLICATION NUMBER: 08/826,847
: PRIOR FILING DATE: April 10, 1997
: PRIOR APPLICATION NUMBER: 60/015,533
: PRIOR FILING DATE: April 10, 1996
: PRIOR APPLICATION NUMBER: 08/903,555
: PRIOR FILING DATE: July 31, 1997
: PRIOR APPLICATION NUMBER: 60/023,308
: PRIOR FILING DATE: July 31, 1996
: PRIOR APPLICATION NUMBER: 08/862,178
: PRIOR FILING DATE: May 22, 1997
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: PRIOR APPLICATION NUMBER: 60/018,217
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: PRIOR APPLICATION NUMBER: 08/881,589
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: PRIOR APPLICATION NUMBER: 60/021,275
: PRIOR FILING DATE: June 25, 1996
: PRIOR APPLICATION NUMBER: 08/903,802
: PRIOR FILING DATE: July 31, 1997
: PRIOR APPLICATION NUMBER: 60/023,308
: PRIOR FILING DATE: July 31, 1996
: PRIOR APPLICATION NUMBER: 08/905,881
: PRIOR FILING DATE: August 1, 1997
: PRIOR APPLICATION NUMBER: 60/025,204
: PRIOR FILING DATE: August 1, 1996
: PRIOR APPLICATION NUMBER: 08/903,471
: PRIOR FILING DATE: July 30, 1997
: PRIOR APPLICATION NUMBER: 60/025,478
: PRIOR FILING DATE: July 31, 1996
: PRIOR APPLICATION NUMBER: 08/903,556
: PRIOR FILING DATE: July 31, 1997
: PRIOR APPLICATION NUMBER: 60/025,217
: PRIOR FILING DATE: August 22, 1996
: PRIOR APPLICATION NUMBER: 08/937,142
: PRIOR FILING DATE: September 23, 1997
: PRIOR APPLICATION NUMBER: 60/026,598
: PRIOR FILING DATE: September 24, 1996
: PRIOR APPLICATION NUMBER: 08/960,746
: PRIOR FILING DATE: October 29, 1997
: PRIOR APPLICATION NUMBER: 60/030,144
: PRIOR FILING DATE: October 30, 1996
: PRIOR APPLICATION NUMBER: 08/826,847
: PRIOR FILING DATE: April 10, 1997
: PRIOR APPLICATION NUMBER: 60/015,533
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: PRIOR APPLICATION NUMBER: 08/755,524
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: PRIOR APPLICATION NUMBER: 60/007,495
: PRIOR FILING DATE: November 22, 1995
: PRIOR APPLICATION NUMBER: 09/021,031
: PRIOR FILING DATE: February 10, 1998
: PRIOR APPLICATION NUMBER: 60/039,325
: PRIOR FILING DATE: February 13, 1997
: PRIOR APPLICATION NUMBER: 09/035,172
: PRIOR FILING DATE: March 4, 1998
: PRIOR APPLICATION NUMBER: 60/040,431
: PRIOR FILING DATE: March 5, 1997
: PRIOR APPLICATION NUMBER: 09/041,894
: PRIOR FILING DATE: March 12, 1998
: PRIOR APPLICATION NUMBER: 60/040,199
: PRIOR FILING DATE: March 14, 1997
: PRIOR APPLICATION NUMBER: 09/050,817
: PRIOR FILING DATE: March 30, 1998
: PRIOR APPLICATION NUMBER: 60/043,792
: PRIOR FILING DATE: April 11, 1997
: PRIOR APPLICATION NUMBER: 09/074,999
: PRIOR FILING DATE: May 8, 1998
: PRIOR APPLICATION NUMBER: 60/048,431
: PRIOR FILING DATE: May 29, 1997
: PRIOR APPLICATION NUMBER: 09/107,592
: PRIOR FILING DATE: June 30, 1998
: PRIOR APPLICATION NUMBER: 60/052,751
: PRIOR FILING DATE: July 1, 1997
: PRIOR APPLICATION NUMBER: 09/094,079
: PRIOR FILING DATE: June 9, 1998
: PRIOR APPLICATION NUMBER: 60/049,975
: PRIOR FILING DATE: June 13, 1997
: NUMBER OF SEQ ID NOS: 35654
: SOFTWARE: PERL Program
: SEQ ID NO 17019
: LENGTH: 295
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:09:50 ; Search time 2238.68 Seconds
(without alignments)
168.259 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18
Sequence: 1 cgttaatcgcgttcctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: GenDb1:*
2: gb_da:*
3: gb_htg:*
4: gb_in:*
5: gb_cm:*
6: gb_ov:*
7: gb_pat:*
8: gb_ph:*
9: gb_pl:*
10: gb_pr:*
11: gb_ro:*
12: gb_sts:*
13: gb_sy:*
14: gb_un:*
15: gb_vl:*
16: em_da:*
17: em_fun:*
18: em_hum:*
19: em_in:*
20: em_mu:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_un:*
30: em_vl:*
31: em_htg_hum:*
32: em_htg_inv:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB	ID	Description
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1	18	100.0	335	8	AF162898	AF162898 Fusarium
2	18	100.0	335	8 <th>AF162899</th> <th>AF162899 Fusarium</th>	AF162899	AF162899 Fusarium
3	18	100.0	336	8 <th>AF162900</th> <th>AF162900 Fusarium</th>	AF162900	AF162900 Fusarium
4	18	100.0	455	8 <th>FOU28159</th> <th>U28159 Fusarium ox</th>	FOU28159	U28159 Fusarium ox
5	18	100.0	455	8 <th>FOU28161</th> <th>U28161 Fusarium ox</th>	FOU28161	U28161 Fusarium ox
6	18	100.0	456	8 <th>AF440527</th> <th>AF440527 Fusarium</th>	AF440527	AF440527 Fusarium
7	18	100.0	456	8 <th>AF440529</th> <th>AF440529 Fusarium</th>	AF440529	AF440529 Fusarium
8	18	100.0	456	8 <th>AF440531</th> <th>AF440531 Fusarium</th>	AF440531	AF440531 Fusarium
9	18	100.0	456	8 <th>AF440532</th> <th>AF440532 Fusarium</th>	AF440532	AF440532 Fusarium
10	18	100.0	456	8 <th>AF440534</th> <th>AF440534 Fusarium</th>	AF440534	AF440534 Fusarium
11	18	100.0	456	8 <th>AF440539</th> <th>AF440539 Fusarium</th>	AF440539	AF440539 Fusarium
12	18	100.0	456	8 <th>AF440540</th> <th>AF440540 Fusarium</th>	AF440540	AF440540 Fusarium
13	18	100.0	456	8 <th>AF440542</th> <th>AF440542 Fusarium</th>	AF440542	AF440542 Fusarium
14	18	100.0	456	8 <th>AF440552</th> <th>AF440552 Fusarium</th>	AF440552	AF440552 Fusarium
15	18	100.0	456	8 <th>AF440561</th> <th>AF440561 Fusarium</th>	AF440561	AF440561 Fusarium
16	18	100.0	456	8 <th>AF440563</th> <th>AF440563 Fusarium</th>	AF440563	AF440563 Fusarium
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19	18	100.0	457	8 <th>AF440560</th> <th>AF440560 Fusarium</th>	AF440560	AF440560 Fusarium
20	18	100.0	457	8 <th>AF440562</th> <th>AF440562 Fusarium</th>	AF440562	AF440562 Fusarium
21	18	100.0	458	8 <th>AF055220</th> <th>AF055220 Fusarium</th>	AF055220	AF055220 Fusarium
22	18	100.0	506	8 <th>AF069310</th> <th>AF069310 Fusarium</th>	AF069310	AF069310 Fusarium
23	18	100.0	520	8 <th>FOU34566</th> <th>U34566 Fusarium ox</th>	FOU34566	U34566 Fusarium ox
24	18	100.0	521	8 <th>AF176656</th> <th>AF176656 Fusarium</th>	AF176656	AF176656 Fusarium
25	18	100.0	531	8 <th>AF242876</th> <th>AF242876 Fusarium</th>	AF242876	AF242876 Fusarium
26	18	100.0	544	8 <th>FOXYRNA</th> <th>X94173 Fusarium ox</th>	FOXYRNA	X94173 Fusarium ox
27	18	100.0	545	8 <th>FOYBIE58</th> <th>X78260 F.oxysporum</th>	FOYBIE58	X78260 F.oxysporum
28	18	100.0	546	8 <th>FOYCB58</th> <th>X78259 F.oxysporum</th>	FOYCB58	X78259 F.oxysporum
29	18	100.0	546	8 <th>FOYCN58</th> <th>X78258 F.oxysporum</th>	FOYCN58	X78258 F.oxysporum
30	18	100.0	616	8 <th>AF322074</th> <th>AF322074 Fusarium</th>	AF322074	AF322074 Fusarium
31	18	100.0	616	8 <th>AF322075</th> <th>AF322075 Fusarium</th>	AF322075	AF322075 Fusarium
32	18	100.0	616	8 <th>AF322076</th> <th>AF322076 Fusarium</th>	AF322076	AF322076 Fusarium
33	18	100.0	636	8 <th>AF443071</th> <th>AF443071 Fusarium</th>	AF443071	AF443071 Fusarium
34	18	100.0	1471	8 <th>FO58RNA</th> <th>Y07991 F.oxysporum</th>	FO58RNA	Y07991 F.oxysporum
35	16.4	91.1	456	8 <th>AF132799</th> <th>AF132799 Fusarium</th>	AF132799	AF132799 Fusarium
36	16.4	91.1	456	8 <th>AF440525</th> <th>AF440525 Fusarium</th>	AF440525	AF440525 Fusarium
37	16.4	91.1	456	8 <th>AF440526</th> <th>AF440526 Fusarium</th>	AF440526	AF440526 Fusarium
38	16.4	91.1	456	8 <th>AF440526</th> <th>AF440526 Fusarium</th>	AF440526	AF440526 Fusarium
39	16.4	91.1	456	8 <th>AF440535</th> <th>AF440535 Fusarium</th>	AF440535	AF440535 Fusarium
40	16.4	91.1	456	8 <th>AF440536</th> <th>AF440536 Fusarium</th>	AF440536	AF440536 Fusarium
41	16.4	91.1	456	8 <th>AF440537</th> <th>AF440537 Fusarium</th>	AF440537	AF440537 Fusarium
42	16.4	91.1	456	8 <th>AF440541</th> <th>AF440541 Fusarium</th>	AF440541	AF440541 Fusarium
43	16.4	91.1	456	8 <th>AF440544</th> <th>AF440544 Fusarium</th>	AF440544	AF440544 Fusarium
44	16.4	91.1	456	8 <th>AF440545</th> <th>AF440545 Fusarium</th>	AF440545	AF440545 Fusarium
45	16.4	91.1	456	8 <th>AF440546</th> <th>AF440546 Fusarium</th>	AF440546	AF440546 Fusarium
					AF440547	Fusarium

ALIGNMENTS

RESULT 1
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LOCUS 335 bp DNA linear PLN 15-NOV-2001
DEFINITION Fusarium oxysporum f. sp. congluticans 5.8S ribosomal RNA gene, partial sequence; Internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION AF162898
VERSION AF162898.1 GI:5690387
KEYWORDS Fusarium oxysporum f. sp. congluticans.
SOURCE Fusarium oxysporum f. sp. congluticans
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum complex.
REFERENCE 1 (bases 1 to 335)
AUTHORS Min, B. R.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji Dong, Chong Ro-Gu, Seoul 110-743, Korea
FEATURES
Location/Qualifiers
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/strain="MAFF 744001"

/db_xref="taxon:100902"
/note="forma specialis: conglutinans"
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rRNA
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BASE COUNT
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ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 335;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
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Db 162 CGTTAATTCGCTTCCTC 179

RESULT 2
AF162899 335 bp DNA linear PLN 04-AUG-1999
LOCUS
DEFINITION
Fusarium oxysporum f. sp. fragariae 5.8S ribosomal RNA gene,
partial sequence: internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence.
AF162899
VERSION
AF162899.1 GI:5690388
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum f. sp. fragariae.
Fusarium oxysporum f. sp. fragariae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE
1 (bases 1 to 335)
AUTHORS
Min, B.R.
TITLE
Direct Submission
JOURNAL
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea
LOCATION/Qualifiers
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misc_RNA
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rRNA
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BASE COUNT
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ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 335;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
|||||
Db 162 CGTTAATTCGCTTCCTC 179

RESULT 3
AF162900 336 bp DNA linear PLN 04-AUG-1999
LOCUS
DEFINITION
Fusarium oxysporum f. sp. raphani 5.8S ribosomal RNA gene, partial
sequence: internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence.
AF162900
VERSION
AF162900.1 GI:5690389

KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum f. sp. raphani.
Fusarium oxysporum f. sp. raphani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE
1 (bases 1 to 336)
AUTHORS
Min, B.R.
TITLE
Direct Submission
JOURNAL
Submitted (28-JUN-1999) Biology, Sangmyung University, 7 Hong Ji
Dong, Chong Ro-Gu, Seoul 110-743, Korea
LOCATION/Qualifiers
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misc_RNA
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 /product="internal transcribed spacer 2"
rRNA
 275..>336
 /product="28S ribosomal RNA"
BASE COUNT
 89 a 81 c 82 g 84 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 336;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
|||||
Db 163 CGTTAATTCGCTTCCTC 180

RESULT 4
F0028159 455 bp DNA linear PLN 08-JUN-1995
LOCUS
DEFINITION
Fusarium oxysporum strain DAOM 213391 internal transcribed spacer
region ITS1, 5.8S ribosomal RNA gene, and internal transcribed
spacer region ITS2. Includes the 5.8S gene.
F0028159
VERSION
U28159.1 GI:852527
KEYWORDS
SOURCE
ORGANISM
Fusarium oxysporum.
Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE
1 (bases 1 to 455)
AUTHORS
Duggal, A.
TITLE
Direct Submission
JOURNAL
Submitted (31-MAY-1995) Arlie Duggal, Forestry, University of
Toronto, 33 Wilcocks St., Toronto, Ontario M5S 3B3, Canada
LOCATION/Qualifiers
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 /db_xref="taxon:5507"
 /note="The fungus was determined by Selfert K.A. and was
 isolated from wilted carnations from Kenya by Tewari J.P."
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 /note="internal transcribed spacer region: ITS1"
misc_RNA
 148..304
 /product="5.8S ribosomal RNA"
 305..455
 /note="internal transcribed spacer region: ITS2"
BASE COUNT
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ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 8; Length 455;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
 |||
 Db 338 CGTTAATTGCGTTCCTC 355

RESULT 5
 FOU28161 455 bp DNA linear PLN 08-JUN-1995
 LOCUS FOU28161
 DEFINITION Fusarium oxysporum strain CBS 171.31 internal transcribed spacer region ITS1, 5.8S ribosomal RNA gene, and internal transcribed spacer region ITS2. Includes the 5.8S gene.

ACCESSION U28161
 VERSION U28161.1 GI:852529
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

REFERENCE 1 (bases 1 to 455)
 AUTHORS Duggal, A.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-1995) Artie Duggal, Forestry, University of Toronto, 33 Wilcocks St., Toronto, Ontario M5S 3B3, Canada

FEATURES
 source 1..455
 /organism="Fusarium oxysporum"
 /strain="CBS 171.31"
 /db_xref="taxon:5507"
 /note="The fungus was isolated and identified by Wollenweber H.W. from Pinus sp. from Germany"
 misc_RNA 1..147
 /note="Internal transcribed spacer region; ITS1"
 rRNA 148..304
 /product="5.8S ribosomal RNA"
 misc_RNA 305..455
 /note="Internal transcribed spacer region; ITS2"
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 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
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 Db 338 CGTTAATTGCGTTCCTC 355

RESULT 6
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 LOCUS AF440527
 DEFINITION Fusarium oxysporum isolate 14RK-11 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

ACCESSION AF440527
 VERSION AF440527.1 GI:18034395
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

REFERENCE 1 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.
 TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum from tomato plants
 JOURNAL Can. J. Bot. (2002) In press
 REFERENCE 2 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.

TITLE Direct Submission
 JOURNAL Submitted (29-Oct-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave., BARC-West, Beltsville, MD 20705, USA

FEATURES
 source 1..456
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 /isolate="14RK-11"
 /db_xref="taxon:5507"
 misc_RNA 1..147
 /product="Internal transcribed spacer 1"
 rRNA 148..305
 /product="5.8S ribosomal RNA"
 misc_RNA 306..456
 /product="Internal transcribed spacer 2"
 BASE COUNT 120 a 124 c 99 g 113 t
 ORIGIN

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
 |||
 Db 339 CGTTAATTGCGTTCCTC 356

RESULT 7
 AF440529 456 bp DNA linear PLN 02-JAN-2002
 LOCUS AF440529
 DEFINITION Fusarium oxysporum isolate 35RK-14 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.

ACCESSION AF440529
 VERSION AF440529.1 GI:18034397
 KEYWORDS
 SOURCE Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

REFERENCE 1 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.
 TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum from tomato plants
 JOURNAL Can. J. Bot. (2002) In press
 REFERENCE 2 (bases 1 to 456)
 AUTHORS Bao, J.R., Fravel, D.R. and Lazarovits, G.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300 Baltimore Ave., BARC-West, Beltsville, MD 20705, USA

FEATURES
 source 1..456
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 /isolate="35RK-14"
 /db_xref="taxon:5507"
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 /product="Internal transcribed spacer 1"
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 BASE COUNT 120 a 124 c 99 g 113 t
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 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgttaattcgcttcctc 18
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 Db 339 CGTTAATTGCGTTCCTC 356

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RESULT      8
AF440531
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DEFINITION  Fusarium oxysporum isolate 44RK-35 internal transcribed spacer 1,
              5.8S ribosomal RNA gene, and internal transcribed spacer 2,
              complete sequence.
ACCESSION   AF440531
VERSION     AF440531.1  GI:18034399
KEYWORDS
SOURCE      Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1 (bases 1 to 456)
AUTHORS    Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE      Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
            from tomato plants
JOURNAL     Can. J. Bot. (2002) In press
REFERENCE   2 (bases 1 to 456)
AUTHORS    Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE      Direct Submission
JOURNAL     Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
            Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  cgttaatcgcttcctc 18
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DB      339  CGTTAATTCGCGTTCCTC 356

RESULT      9
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DEFINITION  Fusarium oxysporum isolate 73RK-1 internal transcribed spacer 1,
              5.8S ribosomal RNA gene, and internal transcribed spacer 2,
              complete sequence.
ACCESSION   AF440532
VERSION     AF440532.1  GI:18034400
KEYWORDS
SOURCE      Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1 (bases 1 to 456)
AUTHORS    Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE      Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
            from tomato plants
JOURNAL     Can. J. Bot. (2002) In press
REFERENCE   2 (bases 1 to 456)
AUTHORS    Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE      Direct Submission
JOURNAL     Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
            Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      339  CGTTAATTCGCGTTCCTC 356

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FEATURES
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  cgttaatcgcttcctc 18
        |||||||
DB      339  CGTTAATTCGCGTTCCTC 356

RESULT      10
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LOCUS       AF440534          456 bp    DNA        linear    PLN 02-JAN-2002
DEFINITION  Fusarium oxysporum isolate AL22 internal transcribed spacer 1, 5.8S
              ribosomal RNA gene, and internal transcribed spacer 2, complete
              sequence.
ACCESSION   AF440534
VERSION     AF440534.1  GI:18034402
KEYWORDS
SOURCE      Fusarium oxysporum.
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
            complex.
REFERENCE   1 (bases 1 to 456)
AUTHORS    Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE      Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
            from tomato plants
JOURNAL     Can. J. Bot. (2002) In press
REFERENCE   2 (bases 1 to 456)
AUTHORS    Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE      Direct Submission
JOURNAL     Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
            Baltimore Ave, BARC-West, Beltsville, MD 20705, USA

FEATURES
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            misc_RNA        306..456
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BASE COUNT   120 a      124 c      99 g      113 t
ORIGIN
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  cgttaatcgcttcctc 18
        |||||||
DB      339  CGTTAATTCGCGTTCCTC 356

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RESULT 11
AF440539 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440539
DEFINITION Fusarium oxysporum isolate DEH1 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440539
VERSION AF440539.1 GI:18034407
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 339 CGTTAATTCGCGTTCCTC 356
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AF440540 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440540
DEFINITION Fusarium oxysporum isolate DEH2 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440540
VERSION AF440540.1 GI:18034408
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
Location/Qualifiers

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misc_RNA
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Best Local Similarity 100.0%; Pred. No. 12;
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OY 1 cgtaatcgcgttcctc 18
|||||
Db 339 CGTTAATTCGCGTTCCTC 356
RESULT 13
AF440542 456 bp DNA linear PLN 02-JAN-2002
LOCUS AF440542
DEFINITION Fusarium oxysporum isolate Fo47 internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence.
ACCESSION AF440542
VERSION AF440542.1 GI:18034410
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 456)
AUTHORS Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
from tomato plants
JOURNAL Can. J. Bot. (2002) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Bao, J. R., Fravel, D. R. and Lazarovits, G.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
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/isolate="Fo47"
/db_xref="taxon:5507"
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BASE COUNT 120 a 124 c 99 g 113 t
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cgtaatcgcgttcctc 18
|||||
Db 339 CGTTAATTCGCGTTCCTC 356
RESULT 14
AF440552

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LOCUS          AF440552          456 bp      DNA      linear      PLN 02-JAN-2002
DEFINITION    Fusarium oxysporum isolate IA7 Internal transcribed spacer 1, 5.8S
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               sequence.
ACCESSION     AF440552
VERSION       AF440552.1  GI:18034420
KEYWORDS
SOURCE
ORGANISM      Fusarium oxysporum.
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
               Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
               complex.
REFERENCE     1 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
               from tomato plants
JOURNAL      Can. J. Bot. (2002) In press
REFERENCE     2 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Direct Submission
JOURNAL      Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
               Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
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               misc_RNA
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgtaatcgagtcctc 18
    |||
Db 339 CGTTAATCGCGTTCCTC 356

RESULT 15
AF440561          456 bp      DNA      linear      PLN 02-JAN-2002
LOCUS          Fusarium oxysporum isolate PE11 Internal transcribed spacer 1, 5.8S
DEFINITION    ribosomal RNA gene, and internal transcribed spacer 2, complete
               sequence.
ACCESSION     AF440561
VERSION       AF440561.1  GI:18034429
KEYWORDS
SOURCE
ORGANISM      Fusarium oxysporum.
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
               Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
               complex.
REFERENCE     1 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Genetic analysis of pathogenic and nonpathogenic Fusarium oxysporum
               from tomato plants
JOURNAL      Can. J. Bot. (2002) In press
REFERENCE     2 (bases 1 to 456)
AUTHORS      Bao,J.R., Fravel,D.R. and Lazarovits,G.
TITLE        Direct Submission
JOURNAL      Submitted (29-OCT-2001) Vegetable Laboratory, USDA-ARS, 10300
               Baltimore Ave, BARC-West, Beltsville, MD 20705, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 339 CGTTAATCGCGTTCCTC 356

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GenCore version 4.5
copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using bw model

Run on: August 21, 2002, 22:22:44 ; Search time 594.49 Seconds
(without alignments)
51.985 Million cell updates/sec

Title: US-10-046-955-50

Sequence: 1 cgtaaattcgcgttcctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	20	AAV83697	Species-specific F
2	18	100.0	382	21	AAV2783	5.8s rRNA gene seq
3	15	83.3	128	23	AA548419	Enterococcus faec
4	15	83.3	250	23	AA547978	Enterococcus faec
5	15	83.2	9212	20	AAV13271	Enterococcus faec
6	14.8	82.2	650	22	AA505503	Mammalian vestib
7	14.8	82.2	1200	23	AB112625	Drosophila melano
8	14.8	82.2	3128	23	AA512683	Enterococcus faec
9	14.8	82.2	3257	23	AB112624	Drosophila melano

[illegible]

ALIGNMENTS

RESULT	1
AAV83697	
ID	AAV83697 standard; DNA; 18 BP.

26-FEB-1999 (first entry)

Species-specific probe targeted to the internal transcribed spacer 2.

A. niger, *A. terreus*, *A. nidulans*, *Fusarium solani*, *F. moniliforme*, *Mucor rouxii*, *M. raeticus*, *M. plumbeus*, *M. indicus*, *A. fumigatus*, *M. circinellus*, *R. circinellus*, *Rhizopus oryzae*, *R. microsporus*, *R. circinellus*, *R. stolonifer*, *Rhizomorces pusillus*, *Abisidia cyclophera*, *Cunninghamella elegans*, *Pseudallescheria boydii*, *Scedosporium apiospermum*, *Cunninghamella notata*, *Sporothrix schenckii*, *Illamamentus fungus*, *ss.*

OS	Synthetic.
OS	Fusarium oxysporum

	location/Qualifiers
FH	Key modified_base
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FT	/*tag" a
FT	/note="labelled with digoxigenin

W09850584-A2

12-NOV-1998

PF 01-MAY-1998; 98WO-US08926

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XX 02-MAV-1997: 97US-0045400.
RC
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Aldorevich L, Chol JS, Morrison CJ, Reiss E;
PI
XX WPI; 1999-034737/03.
DR
XX New nucleic acid probes for filamentous fungi - for detecting e.g.
PT Aspergillus, Fusarium, Mucor, Rhizopus, Rhizomucor, Absidia
PT Cunninghamella, Pseudallescheria boydii, Penicillium and Sporothrix
PT species.
XX
PS Example 1; Page 22; 45pp; English.
XX
XX Probes AAV83677-708 are derived from the internal transcribed spacer 2
CC (ITS2) region of various filamentous fungi (see AAV70845-73). The probes
CC are species-specific, and can be used for identifying a species selected
CC from Aspergillus flavus, A. fumigatus, A. niger, A. terreus, A.
CC nidulans, Fusarium solani, F. moniliforme, Mucor rouxii, M. racemosus, M.
CC plumbeus, M. indicus, M. circinaloides f. circinaloides, Rhizopus
CC oryzae, R. microsporus, R. citranus, R. stolonifer, Rhizomucor
CC pusillus, Absidia corymbifera, Cunninghamella elegans, Pseudallescheria
CC boydii (teleomorph of Scedosporium apiospermum), Penicillium notatum, or
CC Sporothrix schenckii. The probes can be used for differentiating
CC filamentous fungal species from each other and from other medically
CC important fungi.
CC
XX Sequence 18 BP; 2 A; 6 C; 3 G; 7 T; 0 other;
SO
XX
XX Query Match 100.0%; Score 18; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. NO. 2.6;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 cgttaatcgcgttcctc 18
Oy |||||||
XX 1 cgttaatcgcgttcctc 18
Db
XX
XX RESULT 2
XX AAA72783
XX ID AAA72783 standard; DNA; 382 BP.
XX
XX AAA72783:
XX
XX 13-DEC-2000 (first entry)
DX
XX 5.8s rRNA gene sequence.
XX
XX DE 5.8s rRNA gene sequence.
XX
XX Black spot disease; brown spot disease; fungi; fruit vegetable;
XX field crop; Alternaria; 5.8s rRNA; detection; ds.
KW
XX Fusarium oxysporum.
XX
XX WO200046397-A1.
XX
XX 10-AUG-2000.
XX
XX 24-JAN-2000; 2000MO-US01466.
XX
XX 02-FEB-1999; 99US-0241427.
XX
XX (TECR ) TECHNITION RES & DEV FOUND LTD.
PA (KASH/) KASHI Y.
XX
XX Kashi Y, Zur G, Sharf R, Hallerman E;
PI
XX WPI; 2000-499381/44.
XX
XX Nucleic acid based assay and kit for detection of Alternaria
PT contamination in food products involves analysing the sample of food
PT product for nucleic acid sequences unique to Alternaria -

```

The invention relates to a nucleic acid based method for the detection of *Alternaria* contamination in a food product. The method involves obtaining and analysing a food product sample for a nucleic acid sequence unique to *Alternaria*. Detectable levels of the nucleic acid sequence can be used as an indication of *Alternaria* contamination. Fungi from the genus *Alternaria* are ubiquitous saprophytes and are economically important pathogens affecting a wide range of plants. *Alternaria* are the causative agents of black or brown spot disease in many fruits, vegetables and field crops. The method is used for the detection of *Alternaria* contamination in food products. The present sequence CC represents the Fusarium oxysporum 5.8S rRNA gene, used in examples CC illustrating the invention.

Sequence 382 BP; 101 A; 99 C; 87 G; 95 T; 0 other:

Query Match 100.0%; Score 18; DB 21; Length 382;
 Best Local Similarity 100.0%; Pred. NO. 2.7;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgttaattcgcgttcctc 18
 ||||||||||||||||
 Db 287 cgttaattcgcgttcctc 304

RESULT 3
 AAS48419/C
 ID AAS48419 standard; DNA; 128 BP.
 XX
 AC AAS48419;
 XX
 DT 13-FEB-2002 (first entry)
 DE Enterococcus faecalis cellular proliferation inhibitory sequence #989.
 XX
 KW Antisense; ss; prokaryotic cellular proliferation;
 XX antibiotic; antibacterial; drug design.
 XX
 OS Enterococcus faecalis.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US09180.
 PF
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI: 2001-611495/70.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Claim 1; Seq ID No 996; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence is an antisense
CC oligonucleotide of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 128 BP; 42 A; 31 C; 22 G; 33 T; 0 other;

Query Match	83.3%	Score 15;	DB 23;	Length 128;
Best Local Similarity	100.0%	Pred. No. 1.1e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	2	gtcaatcgcgctcc	16
Db	118	grrrAATTCGCGrrcc	104

RESULT	4
AAS47978/c	
ID	AAS47978 standard; DNA; 250 BP.

AC	AAS47978;
XX	
DT	13-FEB-2002 (first entry)

DE Enterococcus faecalis proliferation inhibitory sequence #548.

Antisense; ss; prokaryotic cellular proliferation;
antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 26-MAY-2000; 2000US-207727P.

PR 27-NOV-2000; 2000US-253625P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX

[illegible]

PT antibiotics, comprise sequences of antisense nucleic acids -

PS Claim 1; Seq ID No 555; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence is an antisense
CC oligonucleotide of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC http://wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 250 BP; 75 A; 53 C; 47 G; 75 T; 0 other;

Query Match	83.3%	Score 15;	DB 23;	Length 250;
Best Local Similarity	100.0%	Pred. No. 1.1e+02;		
Matches 15; Conservative 0;		Mismatches 0;	Indels 0;	Gaps 0

QY	2	gttaatcgcgttc	16
Db	54	GTTAATTCGGCTTC	40

RESULT	5
AAAX13271	
ID	AAAX13271 standard; DNA; 9212 BP.

AA	AA
AC	AA
XX	AA
DT	AA

AA	DE	Enterococcus faecalis genome contig	SEQ ID NO:334.
AA	DE	Enterococcus faecalis genome contig	SEQ ID NO:334.

Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds

Enterococcus faecalis.

PN W09850555-A2.

PD 12-NOV-1998

AA
PF 04-MAY-1998; 98WO-US08985.

AA 14-NOV-1997; 97US-0066009.
PR

PR	16-MAY-1997;	97US-0046655.
PR	00-MAY-1997;	97US-0044031.
PR	00-MAY-1997;	97US-0044031.

PA (HUMA-) HUMAN GENOME SCI INC.

Barash SC, Dillon PJ, Kunsch CA;

DR WPI; 1999-045171/04.

PT New isolated *Enterococcus faecalis* polynucleotides and polypeptides
PT - used to develop products for the detection of *Enterococcus* and for
PT use in vaccines for prevention or attenuation of *Enterococcus*
PT infection.

PS Claim 1; Page 1436-1441; 2084pp; English

A computer-readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the *Enterococcus faecalis* genome AA112338 to AA113919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the *Enterococcus faecalis* genome with commercial importance. The products can be used to detect the presence of *Enterococcus faecalis* in samples. They can also be used for

CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.

XX Sequence 9212 BP; 3045 A; 1564 C; 2061 G; 2529 T; 13 other;

Query Match 83.3%; Score 15; DB 20; Length 9212;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 gtaattcgcttc 16
|||||
Db 4989 gtaattcgcttc 5003

RESULT 6

AAS05503
ID AAS05503 standard; DNA; 650 BP.

XX AAS05503;

DT 07-SEP-2001 (first entry)

DE Mammalian vestibular system geotactic behaviour modulator gene #103.

XX Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo;
KM graviperceptive disorder; motion sickness; labyrinthitis; sypnalls; ds;
KM Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy;
KM trauma; infection of the middle ear; ototoxic agent exposure.

XX Drosophila melanogaster .

OS WO200140519-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32639.

XX 02-DEC-1999; 99US-0168579.

PR 26-SEP-2000; 2000US-0669751.

XX (NEUR-) NEUROSCIENCES RES FOUND INC.

PI Greenspan RJ;

DR WPI; 2001-356159/37.

PT New isolated nucleic acid having mammalian vestibular system-modulating
PT activity useful in the treatment of disorders such as motion sickness
PT and vertigo .

XX Claim 59; Page 126; 179pp; English.

CC The sequences shown in AAS05401-AAS0561 represent DNA with mammalian
CC vestibular system-modulating activity. The DNA sequences can be used in a
CC method whereby a first and second strain of an invertebrate is obtained,
CC and both are subjected to conditions in which the strains exhibit
CC different geotactic behaviour. Genes that are differentially expressed in
CC the first strain relative to the second strain are then identified.
CC Mammalian genes having substantially the same nucleic acid sequence as
CC these genes are used to decrease the symptoms of graviperceptive
CC disorders such as motion sickness, vertigo, labyrinthitis, Meniere's
CC disease, acoustic neuroma, multiple sclerosis, sypnalls, trauma,
CC infection of the middle ear, exposure to ototoxic agents and epilepsy.

XX Sequence 650 BP; 182 A; 181 C; 167 G; 120 T; 0 other;

Query Match 82.2%; Score 14.8; DB 22; Length 650;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 cgttaatcgcttc 18
|||||
Db 69 cgtcatacgcttc 86

RESULT 7

ABL12625
ID ABL12625 standard; cDNA; 1200 BP.

XX ABL12625;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32357.

XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

XX P-PSDB; ABB68522.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Claim 1; SEQ ID NO 32357; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABB57737-ABB72072) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://ipo.int/pub/published_pct_sequences.

XX Sequence 1200 BP; 335 A; 319 C; 318 G; 228 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 1200;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 cgttaatcgcttc 18
|||||
Db 75 cgtcatacgcttc 92

RESULT 8

AAS52883/c

ID AAS52883 standard; DNA; 3138 BP.
 AC AAS52883;
 XX
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Enterococcus faecalis DNA for cellular proliferation protein #311.
 XX
 XX Antisense; ds; prokaryotic cellular proliferation gene;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Enterococcus faecalis.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI: 2001-611495/70.
 DR P-PSDB: AA035024.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Claim 27; Seq ID No 6520; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 3138 BP; 1239 A; 554 C; 631 G; 714 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 3138;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
 |||||
 DB 1644 CGTAAATCCGCTTCGC 1627

RESULT 9

ABL12624/C
 ID ABL12624 standard; cDNA; 3257 BP.
 XX
 XX ABL12624;
 AC
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32354.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI: 2001-656860/75.
 DR P-PSDB: ABB68521.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 32354; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
 CC sequences (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 3257 BP; 796 A; 793 C; 717 G; 951 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 3257;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
 |||||
 DB 2183 CGTTCATACGCGTTCCTC 2166

RESULT 10

ABL02050
 ID ABL02050 standard; cDNA; 4491 BP.
 XX
 XX ABL02050;
 AC
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 632.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX

OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB; ABB57947.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1: SEQ ID NO 637; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 4491 BP; 1161 A; 1000 C; 969 G; 1361 T; 0 other;
 XX

Query Match 82.2%; Score 14.8; DB 23; Length 4491;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 cgttaattcgcgttcctc 18
 ||||||||| || |||||
 Db 760 cgttaattcgcgttcctc 777

RESULT 11
 ABL03754
 ID ABL03754 standard; cDNA; 5864 BP.
 XX
 AC ABL03754;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 5744.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PA WO200171042-A2.
 XX
 PI 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX

XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB; ABB59651.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1: SEQ ID NO 5744; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 5864 BP; 1530 A; 1320 C; 1262 G; 1752 T; 0 other;
 XX

Query Match 82.2%; Score 14.8; DB 23; Length 5864;
 Best Local Similarity 78.9%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 cgttaattcgcgttcctc 18
 ||||||||| || |||||
 Db 4942 cgttaattcgcgttcctc 4959

RESULT 12
 ABL02692
 ID ABL02692 standard; cDNA; 15428 BP.
 XX
 AC ABL02692;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2558.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PA WO200171042-A2.
 XX
 PI 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB; ABB58589.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1: SEQ ID NO 2558; 21pp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB85737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
CC
CC
SQ Sequence 15428 BP; 4834 A; 2815 C; 2869 G; 4910 T; 0 other;

Query Match 82.2%; Score 14.8; DB 23; Length 15428;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
|||||
DB 8063 cgttaatcacttcctc 8080

RESULT 13
AAH53833/C
ID AAH53833 standard; DNA: 939 BP.

AC AAH53833;

DT 03-SEP-2001 (first entry)

DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3059.

KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KM vaccination; endocarditis; ds.

OS Staphylococcus epidermidis.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000MO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAXO) GLAXO GROUP LTD.

PI Kimerly MJ;

PT WPI: 2001-316495/33.

DR P-PSDB: AAG82983.

PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
PT useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 805; 2188bp; English.

AAH5304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to
CC AAH5098 represent oligonucleotide sequences and primers which are used

CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
CC
SQ Sequence 939 BP; 322 A; 122 C; 183 G; 312 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 939;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ttaatcgcttcctc 18
|||||
DB 616 TTAATTCAGCTTCCTC 601

RESULT 14
AAH54455
ID AAH54455 standard; DNA: 2815 BP.

AC AAH54455;

DT 03-SEP-2001 (first entry)

DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3819.

KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
KM vaccination; endocarditis; ds.

OS Staphylococcus epidermidis.

PN WO200134809-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000MO-US30782.

PR 09-NOV-1999; 99US-0164258.

PA (GLAXO) GLAXO GROUP LTD.

PI Kimerly MJ;

PT WPI: 2001-316495/33.

PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
PT useful for vaccinating against infections, e.g. endocarditis -

PS Claim 8; Page 1457-1458; 2188bp; English.

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
CC (I) and (II) can have antibacterial activity and therefore can be used
CC in vaccination. The nucleic acids (I) may be used to produce the
CC S. epidermidis polypeptides (II) via the production of vectors
CC containing them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to
CC AAH5098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.

XX
SQ Sequence 2815 BP; 958 A; 518 C; 315 G; 1024 T; 0 other;

Query Match 80.0%; Score 14.4; DB 22; Length 2815;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ttaattcgcttcctc 18
|||||
Db 792 ttaattcgcttcctc 807

RESULT 15

AA071481/C
ID AA071481 standard; cDNA; 3208 BP.

AC AA071481;

DT 01-MAY-1995 (first entry)

DE omp2 locus of Brucella abortus biovar 1 (S2308).

KM omp2; consensus; Brucella; identification; diagnosis; infection;
KW biovar; cattle; disease; ss.

OS Brucella abortus biovar 1 (S2308).

PN US5348857-A.

PD 20-SEP-1994.

PF 22-MAY-1990; 90US-0527017.

PR 22-MAY-1990; 90US-0527017.

PR 06-NOV-1992; 92US-0972791.

PA (TEXA) UNIV TEXAS A & M.

PI Adams LG, Ficht TA;

DR WPI: 1994-302203/37.

PT Identification of Brucella species or biovars - by amplification
of the Brucella omp2 gene locus and hybridisation with DNA probes

PS Disclosure; Columns 17-21; 50pp; English.

CC Rapid detection of Brucella may be achieved by amplifying the omp2
gene locus of Brucella (which shows genetic variation correlating
with established species designations) and hybridising the amplified
sequence with a panel of DNA probes to identify a species of biovar
of Brucella. The amplified sequence is preferably a sequence between
nucleotides 2470 and 3346 of the consensus sequence described in
AA071479. The method is used for the detection of Brucella infection in
animals, particularly humans and cattle.

SO Sequence 3208 BP; 761 A; 864 C; 868 G; 715 T; 0 other;

Query Match 77.8%; Score 14; DB 15; Length 3208;
Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
|||||
Db 1488 GTTAATTCGCTTC 1475

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 22:12:29 ; Search time 138.45 Seconds
(without alignments)
31.935 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcgttcctc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA:*

1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*

2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*

3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*

4: /cgn2_6/prodata/1/lna/6B_COMB.seq:*

5: /cgn2_6/prodata/1/lna/6C_COMB.seq:*

6: /cgn2_6/prodata/1/lna/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	77.8	3208	1	US-07-972-791-3
2	14	77.8	3345	1	US-07-972-791-7
3	14	77.8	3346	1	US-07-972-791-5
4	14	77.8	3347	1	US-07-972-791-2
5	14	77.8	3347	1	US-07-972-791-8
6	14	77.8	3361	1	US-07-972-791-6
7	14	77.8	3434	6	5310649-1
8	13	76.7	5679	4	US-08-844-274-10
9	13	76.7	6723	4	US-08-844-274-13
10	13	76.7	6723	4	US-08-844-274-14
11	13	76.7	7560	4	US-08-844-274-20
12	13	76.7	9717	4	US-09-251-645-1
13	13	76.7	9717	4	US-09-251-645-1
14	13	76.7	3378	1	US-07-972-791-1
15	13	73.3	23	4	US-09-139-617-10
16	13	73.3	471	3	US-09-181-183-1
17	13	73.3	669	3	US-09-277-700-1
18	13	73.3	669	3	US-09-181-183-27
19	13	73.3	1647	4	US-09-277-700-27
20	13	73.3	3346	4	US-09-139-617-2
21	12	71.1	583	4	US-09-972-791-4
22	12	71.1	305	4	US-09-091-725-26
23	12	71.1	627	4	US-09-328-111-218
24	12	71.1	890	4	US-09-385-982-4
25	12	71.1	932	4	US-09-328-111-111
26	12	71.1	1377	1	US-09-328-111-130
27	12	71.1	1377	1	US-08-174-467-20
28	12	71.1	1377	3	US-08-452-071-20

C 28	12.8	71.1	1977	4	US-09-626-589-5	Sequence 5, Appl1
C 29	12.8	71.1	2151	4	US-09-626-589-4	Sequence 4, Appl1
C 30	12.8	71.1	2185	1	US-08-173-508-3	Sequence 3, Appl1
C 31	12.8	71.1	2185	2	US-08-265-310-3	Sequence 3, Appl1
C 32	12.8	71.1	2185	3	US-08-951-742-3	Sequence 3, Appl1
C 33	12.8	71.1	2346	1	US-08-724-298A-1	Sequence 1, Appl1
C 34	12.8	71.1	2472	4	US-09-626-589-6	Sequence 6, Appl1
C 35	12.8	71.1	4579	1	US-08-592-214A-17	Sequence 17, Appl1
C 36	12.8	71.1	4579	3	US-09-149-976-17	Sequence 17, Appl1
C 37	12.8	71.1	5163	3	US-08-700-651-1	Sequence 1, Appl1
C 38	12.8	71.1	5163	3	US-08-928-361B-4	Sequence 4, Appl1
C 39	12.8	71.1	5318	3	US-08-700-651-2	Sequence 2, Appl1
C 40	12.8	71.1	5318	3	US-08-928-361B-3	Sequence 3, Appl1
C 41	12.8	71.1	5511	3	US-08-928-361B-2	Sequence 2, Appl1
C 42	12.8	71.1	7334	3	US-08-928-361B-1	Sequence 1, Appl1
C 43	12.4	68.9	4249	1	US-08-480-784-21	Sequence 21, Appl1
C 44	12.4	68.9	4249	1	US-08-483-553-21	Sequence 21, Appl1
C 45	12.4	68.9	4249	1	US-08-487-002-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-07-972-791-3/C
Sequence 3, Appl1 Application US/07972791
Patent No. 5348657
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING SPECIES AND BIOVARS OF BRUCELLA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3208 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 1 (S2308)
US-07-972-791-3

Query Match 77.8%; Score 14; DB 1; Length 3208;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcggttc 15
|||||
Db 1488 GTTAATTCGCGTTC 1475

RESULT 2

US-07-972-791-7/C
; Sequence 7, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,791
; FILING DATE: 19921106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; TELEX: 792026
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3345 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Brucella melitensis
; STRAIN: biovar 1
; US-07-972-791-7

Query Match 77.8%; Score 14; DB 1; Length 3345;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 gtaattcggttc 15
|||||
Db 1487 GTTAATTCGCGTTC 1474

RESULT 3

US-07-972-791-5/C
; Sequence 5, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER

STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3346 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella neotomae
US-07-972-791-5

Query Match 77.8%; Score 14; DB 1; Length 3346;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 gtaattcggttc 15
|||||
Db 1488 GTTAATTCGCGTTC 1475

RESULT 4

US-07-972-791-2/C
; Sequence 2, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Ficht, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,791
; FILING DATE: 19921106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165

TELEX: 792026
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella abortus
STRAIN: biovar 5
US-07-972-791-2

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 gtaattcgcttc 15
DB 1488 GTTAATTCGCTTC 1475

RESULT 5
US-07-972-791-6/c
Sequence 8, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRES:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3347 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella suis
STRAIN: biovar 1
US-07-972-791-8

Query Match 77.8%; Score 14; DB 1; Length 3347;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
DB 1488 GTTAATTCGCTTC 1475

RESULT 6
US-07-972-791-6/c
Sequence 6, Application US/07972791
Patent No. 5348857
GENERAL INFORMATION:
APPLICANT: Ficht, Thomas A.
APPLICANT: Sowa, Blair A.
APPLICANT: Adams, L. Gary
TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRES:
ADDRESSEE: PRAVEL, GAMBRELL, HEWITT, & KRIEGER
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,791
FILING DATE: 19921106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
TELEX: 792026
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3361 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Brucella ovis
US-07-972-791-6

Query Match 77.8%; Score 14; DB 1; Length 3361;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaattcgcttc 15
DB 1503 GTTAATTCGCTTC 1490

RESULT 7
5310649-1/c
Patent No. 5310649
APPLICANT: Ficht, Thomas A.; Sowa, Blair A.; Adams, L. Gary
TITLE OF INVENTION: METHOD OF DETECTING SPECIES AND BIOVARS
OF BRUCELLA
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/527,017
FILING DATE: 22-MAY-1990
SEQ ID NO: 1;
LENGTH: 3434
5310649-1

Query Match 77.8%; Score 14; DB 6; Length 3434;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaatacgcgttc 15
|||||
DB 1692 GTTAATCGCGTTC 1679

RESULT 8
US-08-844-274-10/c

; Sequence 10, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omathhage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 10
; LENGTH: 5679
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p3el.2 delta
US-08-844-274-10

Query Match 76.7%; Score 13.8; DB 4; Length 5679;
Best Local Similarity 88.2%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcgttc 17
|||||
DB 805 CCTTAATACGCGTTCGT 789

RESULT 9
US-08-844-274-13/c

; Sequence 13, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omathhage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 13
; LENGTH: 6723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Clone p3el.2H/S
US-08-844-274-13

Query Match 76.7%; Score 13.8; DB 4; Length 6723;
Best Local Similarity 88.2%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcgttc 17
|||||
DB 805 CCTTAATACGCGTTCGT 789

RESULT 10
US-08-844-274-14

; Sequence 14, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omathhage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 14
; LENGTH: 6723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:piggyBac/opd
US-08-844-274-14

Query Match 76.7%; Score 13.8; DB 4; Length 6723;
Best Local Similarity 88.2%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcgttc 17
|||||
DB 5919 cgttaatcgcgttcgt 5935

RESULT 11
US-08-844-274-20

; Sequence 20, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omathhage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 20
; LENGTH: 7560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Clone p3el.2Hs/opd
US-08-844-274-20

Query Match 76.7%: Score 13.8; DB 4; Length 7560;
Best Local Similarity 88.2%: Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttct 17
||||| |||||
DB 4357 cgttaatcgcttct 4373

RESULT 12

US-09-251-645-1
; Sequence 1, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9717
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (412)..(1665)
; OTHER INFORMATION: orf1 -46.4 kda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1686)..(2447)
; OTHER INFORMATION: orf2 -28.1kda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2758)..(3318)
; OTHER INFORMATION: orf3 -20.7 kda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3342)..(4118)
; OTHER INFORMATION: orf4 -28.7 kda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4515)..(9269)
; OTHER INFORMATION: orf5 -176 kda
US-09-251-645-1

Query Match 76.7%: Score 13.8; DB 4; Length 9717;
Best Local Similarity 88.2%: Pred. No. 93;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttct 17
||||| |||||
DB 546 cgttaatcgcttct 562

RESULT 13

US-07-972-791-1/c
; Sequence 1, Application US/07972791
; Patent No. 5348857
; GENERAL INFORMATION:
; APPLICANT: Fichtl, Thomas A.
; APPLICANT: Sowa, Blair A.
; APPLICANT: Adams, L. Gary
; TITLE OF INVENTION: NOVEL PROBES AND METHOD FOR IDENTIFYING

;; TITLE OF INVENTION: SPECIES AND BIOVARS OF BRUCELLA
;; NUMBER OF SEQUENCES: 32
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PRAVEL, GAMBRELL, HEMITT, & KRISGER
;; STREET: 1177 West Loop South, 10th floor
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77027

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/972,791
;; FILING DATE: 19921106
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ketelberger, Denise M.
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713-850-0909
;; TELEFAX: 713-850-0165
;; TELEX: 792026
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3378 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-07-972-791-1

Query Match 75.6%: Score 13.6; DB 1; Length 3378;
Best Local Similarity 92.9%: Pred. No. 11e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaaatcgcttc 15
|||||
DB 1519 gtaaatcgcttc 1506

RESULT 14
US-09-139-617-10/c
; Sequence 10, Application US/09139617
; Patent No. 6222015
; GENERAL INFORMATION:
; APPLICANT: WILKINSON, HILARY
; TITLE OF INVENTION: ESTROGEN RECEPTOR
; FILE REFERENCE: 20047Y
; CURRENT APPLICATION NUMBER: US/09/139,617
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/058,271
; EARLIER FILING DATE: 1997-09-08
; EARLIER APPLICATION NUMBER: 60/060,520
; EARLIER FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: HUMAN
US-09-139-617-10

Query Match 73.3%: Score 13.2; DB 4; Length 23;
Best Local Similarity 83.3%: Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgttaatcgcttc 18
||||| |||||
DB 19 cgttaatcgcttc 2


```
RESULT 15
US-09-181-183-1
; Sequence 1, Application US/09181183
; Patent No. 6146866
; GENERAL INFORMATION:
; APPLICANT: VITANEN, PAUL VEIKKO
; APPLICANT: BACOT, KAREN ONLEY
; APPLICANT: JORDAN, DOUGLAS BRIAN
; TITLE OF INVENTION: LUMAZINE SYNTHASE AND
; TITLE OF INVENTION: RIBOFLAVIN SYNTHASE
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,183
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE//DOCKET NUMBER: CL-1083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: mature spinach LS
; US-09-181-183-1

Query Match 73.3%; Score 13.2; DB 3; Length 471;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
|||||
Db 276 CGTTAATTCTGCTTCTC 293
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Search completed: August 21, 2002, 22:12:32
Job time: 5705 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sv model

Run on: August 21, 2002, 21:32:20 : Search time 5019.06 Seconds

(without alignments)
48.405 Million cell updates/sec

Title: US-10-046-955-50

Perfect score: 18

Sequence: 1 cgttaatcgcgcgtctc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.4	85.6	262	12	AZ359925 1M0103B02
C 2	15.4	85.6	277	12	BH452985 B08GA60TF
C 3	15.4	85.6	493	12	AZ498171 1M0335P13
C 4	15.4	85.6	489	12	BH144783 TDBE091TH
C 5	15.4	85.6	740	12	AG042918 Pan trogl
C 6	15.4	83.3	311	9	AW833312
C 7	15.4	83.3	543	10	BI881942 fms9912.x
C 8	15.4	83.3	636	10	BE557132 fkg4909.y
C 9	15.4	83.3	728	10	BE557132 fkg4909.y
C 10	15.4	83.3	1057	12	AC081712
C 11	14.8	82.2	206	12	AZ891070
C 12	14.8	82.2	206	12	AZ891080
C 13	14.8	82.2	303	9	AA785231
C 14	14.8	82.2	388	10	BF490378 AT26843.5
C 15	14.8	82.2	398	10	BE995152
C 16	14.8	82.2	411	9	AI869164 w15b04.x
C 17	14.8	82.2	426	9	AI212546 x8b12a1.f

18	14.8	82.2	430	9	AI946050
19	14.8	82.2	448	12	AQ945783
20	14.8	82.2	457	10	BM130898
21	14.8	82.2	463	10	BM130858
22	14.8	82.2	464	9	AA941852
23	14.8	82.2	481	10	BM130610
24	14.8	82.2	484	12	BH378699
25	14.8	82.2	505	10	BM131033
C 26	14.8	82.2	509	9	AA533012
C 27	14.8	82.2	513	12	CNS07137
C 28	14.8	82.2	527	10	BM130436
C 29	14.8	82.2	574	9	AI488250
C 30	14.8	82.2	578	10	BF491977
C 31	14.8	82.2	585	10	BI984526
C 32	14.8	82.2	594	10	BE978242
C 33	14.8	82.2	598	12	AO657044
C 34	14.8	82.2	615	12	AO733407
C 35	14.8	82.2	642	9	AI657509
C 36	14.8	82.2	651	9	AI108036
C 37	14.8	82.2	651	9	AI1237983
C 38	14.8	82.2	671	10	BF486076
C 39	14.8	82.2	707	10	BF504348
C 40	14.8	82.2	726	10	BF485588
C 41	14.8	82.2	733	10	BF494223
C 42	14.8	82.2	745	10	BF491456
C 43	14.8	82.2	750	10	BF493859
C 44	14.8	82.2	804	10	BF382280
C 45	14.8	82.2	860	12	CNS04KCL

ALIGNMENTS

RESULT 1
AZ359925 262 bp DNA linear GSS 02-OCT-2000
1M0103B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
house musculus.
GSS.
AZ359925.1 GI:10473625

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Bm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std error: 0.00
Plate: 0103 row: B column: 02
Seq primer: CGTTGTAAACGACGCGCGGT
Class: plasmid ends
High quality sequence stop: 262.
Location/Qualifiers

FEATURES

source
1..262
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0103B02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"
/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 97 a 42 c 72 g 51 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 262;
Best Local Similarity 94.1%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 gtaattcgcgtcttc 18
|||||

Db 214 gttatttcgcttctc 198

RESULT 2
BH452985/c 277 bp DNA linear GSS 12-DEC-2001
LOCUS BOHGA60TF BOHG Brassica oleracea genomic clone BOHGA60, DNA
DEFINITION sequence.
ACCESSION BH452985
VERSION BH452985.1 GI:17638696
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 277)
Town, C.D., Van Aken, S., Uterback, T., and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
unpublished (2001)
Other_GSSs: BOHGA60TR
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source Location/Qualifiers
1..277
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHGA60"
/clone_1lb="BOHG"
/note="Vector: PHOS1: Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 82 a 79 c 66 g 50 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 277;
Best Local Similarity 94.1%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 cgttaattcgcgtcttc 17
|||||

Db 94 cgttaattcgcgttctc 78

RESULT 3
A2498171/c 493 bp DNA linear GSS 05-OCT-2000
LOCUS IM0335P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0335P13 F, DNA sequence.
ACCESSION A2498171
VERSION A2498171.1 GI:10675786
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 493)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 385 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0335 row: P column: 13
Seq primer: CGTTCGMAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 493.
Location/Qualifiers
1..493
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0335P13"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 141 a 86 c 136 g 130 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 493;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gttaatcgcgttcctc 18
|||||
Db 383 GTTAATTCGCTTCCTC 367

RESULT 4
BH144783 499 bp DNA linear GSS 16-AUG-2001
DEFINITION TDE0917H CT0G Lycopersicon esculentum genomic clone CT0G30P13, DNA sequence.
ACCESSION BH144783
VERSION BH144783.1 GI:15200046
KEYWORDS GSS.
SOURCE Tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eusteris I; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 499)
van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Romning,C. and Tanksley,S.
Tomato Demethylated Genomic DNA Sequences
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
Tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: Shotgun.

FEATURES
source Location/Qualifiers
1..499
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="CT0G30P13"
/clone_1lb="CT0G"
/tissue_type="Young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 Kb."
BASE COUNT 152 a 108 c 82 g 157 t
ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 499;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gttaatcgcgttcctc 18
|||||
Db 116 GTTAATTCGCTTCCTC 132

RESULT 5
AG042918

LOCUS AG042918 740 bp DNA linear GSS 01-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-021B05.R, genomic survey sequence.
ACCESSION AG042918
VERSION AG042918.1 GI:16571643
KEYWORDS GSS; GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male BAC Library clone:PTB-021B05.R.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
2 (bases 1 to 740)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpsesgsc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..740
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-021B05.R"
/sex="male"
/cell_type="lymphoblast"
/clone_1lb="PTB Chimpanzee Male BAC Library"
BASE COUNT 242 a 129 c 118 g 236 t 15 others
ORIGIN

Query Match 85.6%; Score 15.4; DB 12; Length 740;
Best Local Similarity 94.1%; Pred. No. 6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gttaatcgcgttcctc 18
|||||
Db 614 GTTAATACGCTTCCTC 630

RESULT 6
AM833312 311 bp mRNA linear EST 18-MAY-2000
LOCUS AM833312
DEFINITION RC2-TT0007-011199-011-h07 TT0007 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM833312
VERSION AM833312.1 GI:7927286
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 311)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,T., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL
MEDLINE
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

FEATURES

SOURCE

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC2-TT0007-011
199-011-h076t3-1999-11-01&t=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 69.
Location/Qualifiers

1. 311
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="TT0007"
/dev_stage="Adult"
/note="Organ: testis; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 83 a 52 c 105 g 71 t
ORIGIN

Query Match 83.3%; Score 15; DB 9; Length 311;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ttaatcgcttcctc 18
|||||
Db 245 TTAATCGCTTCCTC 231

RESULT 7

LOCUS

B1881942 543 bp mRNA linear EST 12-OCT-2001
fm89g12.x1 zebrafish Research Genetics C32 fin Danio rerio cDNA

clone 4468054 3' similar to TR:Q9Y4U4 Q9Y4U4 HYPOTHETICAL 164.5 KD
PROTEIN ; mRNA sequence.

ACCESSION B1881942 GI:16089213
VERSION B1881942.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL
COMMENT

Unpublished (1998)
Other-ESTs: fm89g12.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

FEATURES

SOURCE

Email: zbratfish@watson.wustl.edu
CDNA Library Preparation: Ning Wu. CDNA Library Arrayed by: Steve
Johnson. DNA Sequencing by: Washington University Genome Sequencing
Center. Cloning distribution: Research Genetics web address:
http://www.researchgenetics.com/
Seq primer: T7 from Gibco
High quality sequence stop: 447.
Location/Qualifiers

1. 543
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_id="4468054"
/clone_lib="zebrafish Research Genetics C32 fin"
/issue_type="Fin"
/lab_host="Genethogs (HS996, a phage-resistant isolate of
DH10B)."
/note="Vector: pT7T3D-Pac with a modified polylinker;
Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared
from zebrafish(C32) fin, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is non-normalized. Library was
constructed by Ning Wu. NOTE: Clones from this library are
only available thru Research Genetics (www.resgen.com)."
BASE COUNT 203 a 88 c 91 g 161 t
ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 543;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ttaatcgcttcctc 17
|||||
Db 96 TTAATCGCTTCCTC 110

RESULT 8

LOCUS

BE557132 636 bp mRNA linear EST 30-AUG-2000
fk94g09.y1 zebrafish Research Genetics C32 fin Danio rerio cDNA 5'

similar to TR:O75923 O75923 DYSFERLIN ; mRNA sequence.

ACCESSION BE557132 GI:9821557
VERSION BE557132.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE JOURNAL
COMMENT

Unpublished (1998)
Other-ESTs: FK94g09.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbratfish@watson.wustl.edu
CDNA Library Preparation: Ning Wu. CDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University Genome
Sequencing Center. Cloning distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seq primer: T7 from Amersham
High quality sequence stop: 450.

```

FEATURES
  source
    Location/Qualifiers
      1..636
      /organism="Danio rerio"
      /db_xref="taxon:7955"
      /clone_lib="Zebrafish Research Genetics C32 fin"
      /tissue_type="fin"
      /lab_host="GeneHogs (HS996, a phage-resistant isolate of DH10B)"
      /note="Vector: pPTT3D-Pac with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is non-normalized. Library was constructed by Ning Wu. NOTE: Clones from this library are only available thru Research Genetics (www.resgen.com)."
```

BASE COUNT 203 a 129 c 114 g 190 t

ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ttaatcgctctc 17
|||||

DB 18 TTAATTCGCTTCCT 32

RESULT 9
BG723264 728 bp mRNA linear EST 08-MAY-2001
LOCUS 6026908841 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823109 5',
DEFINITION mRNA sequence.
ACCESSION BG723264
VERSION BG723264.1 GI:14002451
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 728)
NIH-MGC http://mgi.ccl.nhl.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palakovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
http://image.llnl.gov
Plate: LLM10732 row: h column: 22
High quality sequence stop: 725.
Location/Qualifiers
1..728
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4823109"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: BluescriptPR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National

```

BASE COUNT 126 a 224 c 236 g 142 t
ORIGIN
  Institutes of Health). Note: this is a NIH_MGC Library."
```

Query Match 83.3%; Score 15; DB 10; Length 728;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taatcgctctc 18
|||||

DB 550 TAAATTCGCTTCCTC 536

RESULT 10
AG081712
LOCUS AG081712 1057 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-078G04.R, genomic survey sequence.
ACCESSION AG081712
VERSION AG081712.1 GI:16633514
KEYWORDS GSS; GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone: PTB Chimpanzee Male
BAC Library clone: PTB-078G04.R.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (sites)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 1057)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB this BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..1057
/organism="Pan troglodytes"
/db_xref="taxon:9596"
/clone="PTB-078G04.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 233 a 232 c 383 g 175 t 34 others

ORIGIN

Query Match 83.3%; Score 15; DB 12; Length 1057;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 gtaatcgctcc 16
|||||

DB 890 GTTAATTCGCTTCCTC 904

RESULT 11
A2991070 206 bp DNA linear GSS 27-APR-2001
LOCUS A2991070

DEFINITION 2M0275N03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0275N03 F, DNA sequence.
ACCESSION A2991070
VERSION A2991070.1 GI:13862297
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 206)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: N column: 03
Seq primer: CTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 206.
Location/Qualifiers
1. 206
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275N03"
/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114|gblAF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 47 a 69 c 44 g 46 t
ORIGIN

Query Match 82.2% Score 14.8; DB 12; Length 206;
Best Local Similarity 88.9% Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
||||| ||| |||||
Db 115 CGTTAATCGCGCTTCCTC 132

RESULT 12
A2991080

LOCUS A2991080 206 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0275P03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0275P03 F, DNA sequence.
ACCESSION A2991080
VERSION A2991080.1 GI:13862307
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 206)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: P column: 03
Seq primer: CTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 206.
Location/Qualifiers
1. 206
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275P03"
/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g114732114|gblAF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 48 a 69 c 44 g 45 t
ORIGIN

Query Match 82.2% Score 14.8; DB 12; Length 206;
Best Local Similarity 88.9% Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttaatcgcgtctc 18
||||| ||| |||||
Db 115 CGTTAATCGCGCTTCCTC 132

RESULT 13

AA785231 303 bp mRNA linear EST 29-JUL-1998
 LOCUS 95h08a1.f1 Aspergillus nidulans 24hr asexual developmental and
 DEFINITION vegetative cDNA lambda zap library Emericella nidulans cDNA clone
 95h08a1 3', mRNA sequence.
 ACCESSION AA785231
 VERSION AA785231.1 GI:2845399
 SOURCE EST.
 ORGANISM Emericella nidulans.
 Emericella nidulans.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; Emericella.
 REFERENCE 1 (bases 1 to 303)
 AUTHORS Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R.,
 Prade, R. and Roe, B.
 TITLE An Aspergillus nidulans EST Database
 JOURNAL Unpublished (1998)
 COMMENT Other-ESTs: 95h08a1.r1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Partington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 We anticipate the future release of the cDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: M13-20
 High quality sequence stop: 185.
 Location/Qualifiers
 1..303
 /organism="Emericella nidulans"
 /strain="FGSC A26"
 /db_xref="taxon:162425"
 /clone="95h08a1"
 /clone_lib="Aspergillus nidulans 24hr asexual
 developmental and vegetative cDNA lambda zap library"
 /tissue_type="vegetative mycelia, asexual structures"
 /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 3' end of cDNA cloned into XhoI site of pBluescript"
 BASE COUNT 85 a 90 c 65 g 63 t
 ORIGIN

Query Match 82.2%; Score 14.8; DB 9; Length 303;
 Best Local Similarity 88.9%; Pred. No. 1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttaattcggtctc 18
 ||||| |||||
 Db 87 CTTTAATCGCGTTCCTC 104

RESULT 14
 BF490378 388 bp mRNA linear EST 23-APR-2001
 LOCUS AT26843.5prtime AT Drosophila melanogaster adult testes potb7
 DEFINITION Drosophila melanogaster cDNA clone AT26843 5 similar to CG7251:
 Fban000751 located on: 2L 25F1-25F1; 04/09/2001, mRNA sequence.
 ACCESSION BF490378
 VERSION BF490378.2 GI:13756100
 SOURCE EST.
 ORGANISM Drosophila melanogaster
 fruit fly.
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 388)
 AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman
 , B., Carlson, J., Champagne, M., Chavez, C., Chew, M., Dorsett, V., Farfan
 , D., Frisbe, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P.,
 Liao, G., Miranda, A., Mista, S., Mungall, C. J., Nunoo, J., Pacleb, J.,

Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S. E.,
 Celniker, S. and Rubin, G. M.
 BDCP/HMT AT Drosophila EST Project
 JOURNAL Unpublished (2000)
 COMMENT On Dec 6, 2000 this sequence version replaced gi:11573689.
 Contact: Stapleton, M.
 BDCP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
 hit genomic AB003610: arm.2L [5357975,5614606]
 estimated-cyto:25E2-25F4: 04/09/2001
 Plate: AT 268 row: D column: 7
 High quality sequence stop: 334.
 Location/Qualifiers
 1..388
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="AT26843"
 /clone_lib="AT Drosophila melanogaster adult testes potb7"
 /sex="male"
 /dev_stage="0-3 day old Ore-R males"
 /lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
 AT.121-AT.319: DH5-alpha TONA"
 /note="Organ: ADULT testes; Vector: potb7; Site.1: EcoRI;
 Site.2: XhoI; The mRNA for the testis library was made
 from testes and seminal vesicles hand dissected from 0-3
 day old Ore-R males. RNA kindly provided by the lab of
 Margaret Fuller. Sized fractionated cDNAs were directly
 ligated into potb7. Plasmid cDNA library."
 BASE COUNT 103 a 109 c 85 g 91 t
 ORIGIN

Query Match 82.2%; Score 14.8; DB 10; Length 388;
 Best Local Similarity 88.9%; Pred. No. 1e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgttaattcggtctc 18
 ||||| |||||
 Db 82 CTTTAATCGCGTTCCTC 99

RESULT 15
 BE995152 398 bp mRNA linear EST 05-OCT-2000
 LOCUS UI-M-CG0P-b11-g-02-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
 DEFINITION UI-M-CG0P-b11-g-02-0-UI 3', mRNA sequence.
 ACCESSION BE995152
 VERSION BE995152.1 GI:10679108
 SOURCE EST.
 ORGANISM house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 398)
 AUTHORS Bonaldo, M. F., Lennon, G. and Soares, M. B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mesf@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the retina tissue cDNA library preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 1-22,
>AT-rich#low_complexity
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source

Location/Qualifiers
1. .398
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0P-D11-9-02-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.
TAG_LIB=NIH_BMAP_Ret4_S2
TAG_TISSUE=adult-retina
TAG_SEQ=GTGAGCGCGCAC"
BASE COUNT 73 a 96 c 137 g 91 t 1 others
ORIGIN

Query Match 82.2%; Score 14.8; DB 10; Length 398;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cgttaatcgcttcctc 18
||||| ||| |||||
DB 42 CGTTAATCGCGCTTCCTC 25

Search completed: August 21, 2002, 21:32:27
Job time: 12526 sec